FAMILY-SPECIFIC DIFFERENCES IN GROWTH RATE AND HEPATIC GENE EXPRESSION IN TRIPLOID GROWTH HORMONE (GH) TRANSGENIC ATLANTIC SALMON (SALMO SALAR L.)

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Family-specific differences in growth rate and hepatic gene expression in triploid growth hormone (GH) transgenic Atlantic salmon (*Salmo salar* L.)

by

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ABSTRACT

Growth hormone transgenic (GHTg) Atlantic salmon have enhanced growth when compared to their non-transgenic counterparts, and this trait is beneficial for aquaculture production. However, there are concerns regarding the potential impacts of transgenic fish on wild populations. The culture of sterile triploid GH transgenic (3NGHTg) Atlantic salmon would prevent interbreeding of transgenic fish and wild stocks, thus minimizing environmental impacts. Generally, the growth performance of triploid salmon relative to diploid siblings remains an area of investigation. Growth rate of 3NGHTg Atlantic salmon families were found to significantly vary between families in a breeding program. In order to identify gene expression correlates of enhanced growth in 3NGHTg Atlantic salmon, a functional genomics approach (32K cDNA microarrays followed by QPCR) was used to identify and validate liver transcripts that are differentially expressed between two fast-growing 3NGHTg Atlantic salmon families (AS11, AS26) and one slow-growing 3NGHTg Atlantic salmon family (AS25). Of 687 reproducibly informative microarray features, 143 features (116 more highly expressed in fast-growing, and 27 more highly expressed in slow-growing) were identified in the AS11 vs. AS25 microarray study, while 544 features (442 more highly expressed in fast-growing and 102 more highly expressed in slow-growing) were identified in the AS26 vs. AS25 microarray study. In order to identify growth-relevant transcripts that were consistently differentially expressed between fast-growing and slow-growing 3NGHTg families, the AS11 vs. AS25 and AS26 vs. AS25 microarray gene lists were further analyzed using Venn diagrams. Forty microarray features (39 associated with fast growth and 1 associated with slow

growth) were present in both microarray comparisons. The expression levels of 15 microarray-identified transcripts were studied using QPCR with individual RNA samples to validate the microarray results and to study biological variability of transcript expression. The QPCR results agreed with the microarray results for 12 of 13 putative fast-growth associated transcripts, but QPCR did not validate the microarray results for 2 putative slow-growth associated transcripts. Many of the 39 microarray features that were consistently associated with fast-growing 3NGHTg salmon (including ACBP, APOAI, APOAIV, B2M, D5DP, FTM, GAPDH, and NUPR1) were involved in carbohydrate, lipid, and amino acid metabolism, iron homeostasis and oxygen transport, and immune- or stress-related responses. The results of this study increase our knowledge of family-specific impacts on growth rate and hepatic gene expression in 3NGHTg Atlantic salmon. In addition, this study provides a suite of rapid growth rate associated transcripts that may lead to the development of molecular markers (e.g. intronic, exonic or regulatory region SNPs) for the selection of GHTg Atlantic salmon broodstock that will give rise to sterile triploids of desired growth performance for future commercial applications.

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LIST OF ABBREVIATIONS

Abbreviation	Full name
AA5	Annexin
ACBP	Acyl-CoA-binding protein
ADAMTS1	A disintegrin and metalloprotease with thrombospondin motifs-1
AFP	Antifreeze protein
ANOVA	Analysis of variance
APOAI	Apolipoprotein A-I
APOAIV	Apolipoprotein A-IV
B2M	Beta-2 microglobulin
BCLN	Background corrected Lowess normalized
BLAST	Basic local alignment search tool
CCAC	Canadian Council on Animal Care
cDNA	complementary DNA
cGRASP	consortium for Genomic Research on All Salmonids Project
C_T	Cycle threshold
D5DP	Delta-5-desaturase-like protein
D6DP	Delta-6-desaturase protein
Deg-min	Degree minutes
DHA	Docosahexaenoic acid

EPA	Eicosapentaenoic acid
ESTs	Expressed sequence tags
FTM	Ferritin middle subunit
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GDH	Glutamate dehydrogenase
GHTg	Growth hormone transgenic
GO	Gene ontology
TOI	Transcript of interest
GPx	Glutathione peroxidase
GRASP	Genomic Research on Atlantic salmon Project
GS	Glutamine synthetase
IACC	Institutional Animal Care Committees
MHC1	Major histocompatibility complex class I
mRNA	Messenger RNA
NCBI	National Center for Biotechnology Information
NTC	No-template control
NUPR1	Nuclear protein 1
PABP1	Polyadenylate-binding protein 1
PCR	Polymerase chain reactions
PFK	6-phosphofructokinase
PIT	Passive integrated transponder
Psi	Pounds per square inch

QPCR	Quantitative reverse transcription-polymerase chain reaction
RNA-seq	RNA-sequencing
RQ	Relative quantity
rRNA	Ribosomal RNA
SEM	Standard error of mean
SEPP	Selenoprotein Pa precursor
SGR_L	Length-specific growth rate
SGR_W	Weight-specific growth rate
SNPs	Single nucleotide polymorphisms
TIF	Tagged image file
2N	Diploid
3N	Triploid

LIST OF APPENDICES

CO-AUTHORSHIP STATEMENT

The research described in this thesis was carried out by Qingheng Xu under the supervision of Dr. Matthew L. Rise. Additional guidance was provided by Charles Y. Feng and Dr. Tiago S. Hori (members of the Rise lab and collaborators on this project). Qingheng Xu was responsible for conducting experiments, data analysis and thesis writing. The following people and institutions contributed to the research with intellectual and labour inputs:

Charles Y. Feng[1]: provided RNA integrity results, conducted the gene ontology term enrichment analysis, and developed 6 of 15 QPCR assays in families AS11 and AS25; edited and provided comments on the thesis.

Tiago S. Hori[1]: provided training in microarray experimental procedures; edited and provided comments on the thesis.

Debbie A. Plouffe[2] **and John T. Buchanan**[3]: responsible for fish husbandry; fish sampling; collection of data for growth rate determination; ploidy and transgenesis determination; provided comments on the thesis.

Matthew L. Rise[1]: supervised the entire study; edited and provided comments on the thesis.

This will also be the author line of a manuscript based on my M.Sc. thesis that will be submitted for publication in a peer-reviewed journal (e.g. *Aquaculture*).

Additional notes: Results in Appendices VII-XV are from studies conducted by Qingheng Xu; however, they are not the primary focus in this thesis. These results contribute to a

manuscript (entitled "Impact of triploidization on the hepatic transcriptome of growth hormone transgenic Atlantic salmon") that will be submitted for publication in a peer-reviewed journal (e.g. *Marine Biotechnology*). The authorship of this publication will be **Charles Y. Feng[1], Qingheng Xu[1], Tiago S. Hori[1], Debbie A. Plouffe[2], John T. Buchanan[3], and Matthew L. Rise[1]**.

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1. INTRODUCTION

1.1 Growth hormone (GH) transgenesis of fish

1.1.1 Impact of GH transgenes on fish growth performance

In the past few years, due to continually decreasing wild fish stocks (Myers et al., 1997; Myers and Worm, 2003) and increasing demand of fish for human consumption, there has been a large expansion of the aquaculture industry (Bostock et al., 2010; Liu and Sumaila, 2008; Naylor and Burke, 2005). However, the demand continues to grow as human population increases. For this industry to meet the increased demand, it is important to develop technologies that can enhance aquaculture production. Transgenesis is a gene transfer technology that results in the integration of gene(s) of interest into an organism's genome, changing its genotype and phenotype for desired purposes (e.g. enhanced growth, increased freeze resistance or disease resistance of fish) (Hew and Fletcher, 2001; Hew et al., 1995; Zbikowska, 2003). For example, growth hormone (GH) transgenes are able to improve the growth rate of various commercially important fish species, such as Atlantic salmon (*Salmo salar*) and coho salmon (*Oncorhynchus kisutch*) (Devlin et al., 1994; Du et al., 1992). The current study involved GH transgenic (GHTg) Atlantic salmon (*AquAdvantage*® salmon) that were previously generated using a gene construct that contained regulatory sequences from an ocean pout (*Macrozoarces americanus*) antifreeze protein (AFP) gene and coding sequence from Chinook salmon (*Oncorhynchus tshawytscha*) growth hormone gene (Butler and Fletcher, 2009). The AFP

gene promoter drives expression of the GH gene in the GH transgene construct, and this promoter can be regulated (i.e. switched on) by common transcription factors in most fish species (Hew and Fletcher, 2001). Moreover, this promoter can be detected in a host by PCR with ease since most commercially important fish (e.g. salmon, carp, catfish and tilapia) lack AFP gene in their genomes (Hew and Fletcher, 2001). The average weight of the GH transgenic Atlantic salmon was 2-4 times higher than non-transgenic siblings in their first year and they reach market size one year earlier, thereby significantly shortening the production cycle (Du et al., 1992; Fletcher et al., 2004).

In GHTg salmonids, elevated GH expression modifies a number of pathways mostly through GH-mediated signaling, resulting in changes in feeding behavior (e.g. Abrahams and Sutterlin, 1999; Devlin et al., 1999), metabolism (e.g. Cook et al., 2000; Leggatt et al., 2009; Rise et al., 2006), and development (e.g. Devlin et al., 2000). The effects of GH transgenesis on growth rate are thought to be largely determined by genetic background, as a study in rainbow trout (*Oncorhynchus mykiss*) showed that GH transgenesis (construct *OnMTGH1*) enhanced the growth rate in slow-growing wild strains while having very little impact on the growth rate of fast-growing domesticated (direct selected) strains (Devlin et al., 2001). Furthermore, a recent transcriptomic study showed that both domestication and GH-transgenesis modified a set of common pathways involved in growth-related regulation (e.g. protein synthesis, cell/tissue structure, energy production, metabolism) in coho salmon muscle and liver tissues (Devlin et al., 2009). Given the consistency in molecular mechanisms underlying fast growth observed between GH transgenic and domesticated coho salmon strains, it is likely that at least one of these pathways may also play important roles in regulation of growth in triploid salmon.

1.1.2 Obstacles to large-scale commercial aquaculture

GHTg fish are potentially attractive technology products for the development of the aquaculture industry. However, there are important issues to be addressed for GHTg fish to become commercially viable. For example, it is necessary to assess the potential safety issues related to the development and use of this technology and its potential environmental impacts (Fletcher et al., 2004). There is a concern that transgenic fish may accidentally escape from rearing cages and interbreed with wild fish populations, thus potentially posing threats to the natural environment (Moreau et al., 2011; Muir, 2004). To predict the risk, interactions between transgenic fish and cultured/wild non-transgenic fish have been investigated in a mimic natural environment. Such studies have shown that GHTg coho salmon exhibited reduced survival and growth rate when food was scarce (Sundstrom et al., 2004), and had limited reproductive opportunities and abilities when compared with wild coho salmon (Fitzpatrick et al., 2011). Although these findings suggest a low impact of GHTg escapees on the wild fish populations, it is beneficial to have a reliable and controllable approach that can minimize or eliminate any possible interactions between transgenic fish and wild populations and be used for large-scale application of GH transgenic fish in the future.

1.2 Triploidization of fish

1.2.1 Induction of triploidization

In past years, there has been concern and speculation regarding the potential genetic impacts of escaped farmed fish on the fitness of native populations (Hindar et al., 2006; McGinnity et al., 1997; Moreau et al., 2011). A land-based culture of domesticated fish (including transgenics) would be advantageous to reduce the impacts, but it cannot prevent unlicensed breeding of commercial breeds. Therefore, it would be preferable for domesticated fish (including transgenics) reared either in land-based facilities or in sea cages to be reproductively sterile. Among the efforts that have been made in confinement of transgenic fish, triploidization technology, which renders the fish reproductively sterile, is approved to be a practical and effective approach to not only reduce negative effects of sexual maturation on fish production (e.g. weight loss, less desirable flesh quality) (Felip et al., 2001; Thorgaard and Gall, 1979), but also effectively minimize genetic interactions between gene-modified fish and wild populations (Cotter et al., 2000).

Triploidization results in the retention of the second polar body of fertilized eggs during meiosis II division and thus adds an extra set of chromosomes to the fish genome (Swarup, 1959). With an extra set of chromosomes, triploids have nucleus and cell sizes that are proportionally increased to approximately 1.5 times larger than the corresponding cells in diploids; however, the sizes of triploids' organs remain similar to the diploids as a result of compensated cell number (Aliah et al., 1990; Small and Benfey, 1987).

Triploidization can be achieved by applying a thermal shock, hydrostatic pressure, or chemical shock to diploid fish eggs shortly after fertilization (Benfey and Sutterlin, 1984; Chourrout, 1980; Johnstone, 1985; Solar et al., 1984). Among these methods, heat treatment is slightly more effective than cold treatment for coldwater species such as salmonids, while hydrostatic pressure shock generally shows the most consistent results for Atlantic salmon and rainbow trout (Reviewed in Ihssen et al., 1990). Various methods have been developed to determine triploidy (Maxime, 2008) as triploids and diploids are mostly indistinguishable in external appearance (Aliah et al., 1990; Thorgaard and Gall, 1979). Flow cytometry methods employed in the current study allow rapid and accurate determination of ploidy by analyzing the DNA content in fish red blood cells (Maxime, 2008; Thorgaard et al., 1982).

1.2.2. Growth performance of triploid fish

The impact of triploidization on the growth performance of teleost fish has been intensively investigated (Reviewed in Tiwary et al., 2004). It has been hypothesized that somatic growth of reproductively sterile triploid fish is increased as their energy contribution to gonadal development is greatly reduced (Felip et al., 2001; Piferrer et al., 2009). However, in Atlantic salmon, studies on growth performance of triploids are equivocal regarding the impact of triploidization on growth. For example, lower survival and growth rate (McGeachy et al., 1995) and higher incidence of deformity (Benfey, 2001; O'Flynn et al., 1997) have been observed in triploid Atlantic salmon in comparison to their diploid counterparts, while accelerated growth rate in triploid Atlantic salmon has

also been reported (Galbreath et al., 1994). The previously published growth performance response of Atlantic salmon to triploidization may partially be affected by different rearing conditions (e.g. separated or co-existed rearing of diploids and triploids), but is also likely to have been influenced by genetic background of fish strains; evidence from rainbow trout, brown trout (*Salmo trutta*), and chinook salmon shows a significant correlation between genetic background and growth performance (Bonnet et al., 1999; Johnson et al., 2004). In addition, other studies have shown that variability in growth performance is consistently higher among triploid Atlantic salmon families than among their diploid counterparts (Friars et al., 2001; Johnson et al., 2007). In the current study, growth data suggested that growth performance of the diploid Atlantic salmon during 45 days did not necessarily correlate with their triploid counterparts. These observations suggest that triploidization may be an additional source of variability added to genetic diversity that further complicates the study of the genetic/molecular basis of growth rates in these fish. It is therefore of great interest to select diploid broodstock that are optimal for triploid production based on the performance of their triploid offspring. In the current study, I used a functional genomics approach to identify candidate enhanced growth-associated transcripts and pathways that may be valuable in the future development of molecular markers for the selection of GHTg broodstock that will produce rapidly growing 3NGHTg families.

It is important to note that, due to a putative genome duplication event and subsequent partial re-diploidization in the salmonid lineage, modern salmonid genomes are considered to be pseudotetraploid (Davidson et al., 2010); however, to improve readability of this thesis, the Atlantic salmon genome is referred to as diploid.

1.3 Functional genomics tools and techniques

1.3.1 DNA microarrays

DNA microarrays are global gene expression profiling tools. DNA microarrays allow researchers to determine transcript (mRNA) expression levels of thousands of genes simultaneously, and lead us to a thorough understanding of gene activities involved in various biological processes that are vital for aquaculture development. For salmonids, DNA microarray platforms have been developed since 2004. For example, an approximately 3,500 gene (3.5K) salmonid cDNA microarray (Rise et al., 2004b) and a 16K salmonid cDNA microarray (von Schalburg et al., 2005) were produced by the Genomic Research on Atlantic Salmon Project (GRASP). They were employed in published studies to characterize gene expression that was involved in salmonid growth (e.g. Gahr et al., 2008; Rise et al., 2006; Tymchuk et al., 2009), immune response to pathogens (e.g. Morrison et al., 2006; Rise et al., 2004a; Workenhe et al., 2009), and exposure to chemicals (e.g. Gallagher et al., 2008; Gunnarsson et al., 2007). The current study utilized a 32K salmonid cDNA microarray platform for gene expression profiling experiments; this 32K microarray, developed by the consortium for Genomic Research on All Salmon Project (cGRASP), contains 27,917 Atlantic salmon and 4,065 rainbow trout cDNA features as well as control features (e.g. Alien oligonucleotide from Stratagene SpotReport Alien cDNA Array Validation system) (Koop et al., 2008). Recently, a 44K salmonid oligonucleotide (oligo) microarray was produced from cGRASP based on ~500K Atlantic salmon ESTs and ~250K rainbow trout ESTs (Koop et al., 2008).

One of the goals of the cGRASP project was to create tools such as DNA microarrays for functional genomics studies involving Atlantic salmon, rainbow trout and other salmonids; these resources were used extensively in my M.Sc. project. By employing the 32K cGRASP cDNA microarray platform in concert with publicly available nucleotide and amino acid sequence databases (e.g. National Centre for Biotechnology Information (NCBI): http://www.ncbi.nlm.nih.gov, Swiss-Prot Protein Knowledgebase: http://www.uniprot.org), expression profiles of growth-related genes in fast-growing and slow-growing 3NGHTg Atlantic salmon families were studied and differentially expressed genes were annotated. The genes that I identified in microarray experiments as differentially expressed in fast-growing and slow-growing 3NGHTg families may indicate altered molecular pathways involved in various growth-related biological processes. These results will therefore improve our understanding of the genetic basis of variable growth rates in 3NGHTg Atlantic salmon. In addition, identifying genes associated with enhanced growth at the transcript expression level may lead to the development of markers (e.g. single nucleotide polymorphisms (SNPs) in introns, exons, and regulatory regions) for marker assisted selection. The next phase of this research (beyond the scope of this M.Sc. project) will involve mining RNA-sequencing (RNA-seq) data for SNPs in growth-relevant cDNA sequences that may be suitable molecular biomarkers for the selection of GHTg broodstock that will produce rapidly growing 3NGHTg families.

1.3.2. QPCR

Quantitative reverse transcription - polymerase chain reaction (QPCR) is a functional genomics technique that quantifies mRNA expression levels of genes of interest with high sensitivity and accuracy. It involves the conversion of mRNA to cDNA (reverse transcription) and quantification of the level of the mRNA in the sample through exponential amplification by PCR. QPCR has been used to study expression of genes that are important for various biological processes in fish and can allow the researcher to verify the expression levels of genes that have been identified in microarray studies (e.g. Goetz et al., 2009; Morais et al., 2011; Rise et al., 2006; Workenhe et al., 2009). In this study, I utilized QPCR to determine the relative expression levels of microarray-identified transcripts of interest (TOIs) in liver from individual fish to assess biological variability of expression and to validate a subset of the microarray-identified genes.

1.4 Objectives of study

Previous studies of teleost fish have identified several biological processes and pathways that can be affected by GH transgenes (Devlin et al., 2009; Leggatt et al., 2009; Rise et al., 2006); these effects are thought to be influenced by genetic background of the fish strain (Devlin et al., 2001). Given that growth rate is a heritable trait for Atlantic salmon (Reviewed in Garcia de Leaniz et al., 2007), I hypothesize that **growth performance of 3NGHTg Atlantic salmon is associated with their genetic backgrounds, which have strong influences on expression levels of growth-relevant genes in various molecular pathways**.

In this study, six passive integrated transponder (PIT)-tagged 3NGHTg Atlantic salmon families were assessed for weight and length at initial and final time points (approximately 45 days apart). The weight-specific growth rate (SGR_W) and length-specific growth rate (SGR_L) indicated significant variability of growth performance between families. A functional genomics approach was used to identify and validate hepatic transcripts that are associated with growth performance in 3NGHTg Atlantic salmon. The constitutive hepatic transcriptome of two families of fast-growing 3NGHTg Atlantic salmon were compared to that of a family of slow-growing 3NGHTg Atlantic salmon in two independent microarray comparisons using the 32K cGRASP cDNA microarray platform (Koop et al., 2008). Fifteen microarray-identified genes with growth-relevant functional annotations were selected for QPCR study to validate the microarray results and to assess the biological variability of transcript expression.

1.5 Hepatic transcript expression studies in 2N and 3N GHTg Atlantic salmon

While the primary focus of my M.Sc. research was on hepatic gene expression correlates of differential growth rate among 3NGHTg Atlantic salmon families, I also used microarrays and QPCR to investigate the impact of triploidization on hepatic transcript expression in GHTg Atlantic salmon. Global transcript expression in liver tissues of three diploid GHTg salmon families (AS11, AS25, and AS29) was compared to that of the corresponding triploid families using the 32K cDNA microarray platform following the same procedures used for the primary growth-related study. The triploidization microarray experimental design and overview of results are shown in

Appendix XIV. Families AS11, AS25, and AS29 were selected for the triploid versus diploid gene expression analyses due to enhanced or depressed growth performances post-triploidization (Appendix XIII). This research will not only help us to understand the underlying mechanisms of the impact of triploidization on GHTg Atlantic salmon families, but will also offer an opportunity to test correlation in growth performance between diploids and triploids. As a result, hepatic transcripts up-regulated or down-regulated by triploidization, and biological processes associated with these transcripts, were identified (Appendix VII-XII). Some of the informative transcripts identified in the triploid vs. diploid microarray experiment were further studied using QPCR with individual liver samples to validate microarray results and to assess the biological variability in different GHTg families (Appendix XV). The microarray and QPCR data related to the impact of triploidization on the hepatic constitutive transcriptome will contribute to a manuscript (for submission to a peer-viewed journal) on which I am the second author. The authorship and contributions to this research are clarified in the Co-authorship statement.

2. MATERIALS AND METHODS

2.1 Fish husbandry and family selection

All experiments were conducted following the Canadian Council on Animal Care (CCAC) guidelines and were approved by Institutional Animal Care Committees (IACC) of both AquaBounty and Memorial University of Newfoundland.

In this study, each of 19 families of GHTg Atlantic salmon was obtained by fertilization of eggs from a non-transgenic female Atlantic salmon with milt from a hemizygous (i.e. having one copy of the growth hormone transgene) *AquAdvantage*® (AquaBounty Canada, Fortune, Souris, PE) male. For each family, one-half volume of the fertilized eggs was treated with hydrostatic-pressure (9500 pounds per square inch (psi) for a period of five minutes at 300 degree minutes (deg-min) post-fertilization) to induce triploids. The eggs were incubated in stacked incubation trays (10 L) until hatch when the yolk-sac fry were transferred to individual tanks in the early rearing area. The yolk-sac fry were first cultured in a flow-through system and then moved to a recirculation system when they reached ~1 g in weight. Fish of different ploidy were cultured separately in combi-tanks (500 L for early sac-fry or 1500 L for later stages). Density in the tanks was maintained at < 1 kg m^{-3}. Fish were reared with 24 hours light and fed to satiation with a commercial salmon diet of appropriate composition and pellet size at different developmental stages (e.g. Skretting Nutra ST, Nutra Fry, & Optiline (1.0 – 4.0 mm), Vancouver, BC). The water temperature was maintained at 13°C and dissolved oxygen

was kept >90% of air saturation. Approximately 95 days after first feeding (May 20-26, 2009), 50 fish from each family were assessed for weight, length, and visible deformities. Based on this assessment, three families with larger body size and three families with smaller body size were selected from the 19 families. At the initial time point (t_1; July 27-29, 2009), 18 fish selected from each of these six families were PIT-tagged. These fish were then assessed for weight, length, and visible deformities before being evenly distributed into three 500 L tanks (6 fish/family/tank; a total of 36 fish per tank). Approximately 45 days later at the final time point (t_2; September 9-10, 2009; tissue sampling for functional genomics study), nine fish were arbitrarily selected from each of the six families, with three fish from each of the triplicate tanks, had their PIT tags read and were assessed for weight, length, and visible deformities followed by tissue sampling. For family AS29, AS26, and AS33, one additional fish (for a total of 10 fish) was assessed and sampled to ensure a minimum of three females and three males (based on gross gonad morphology) within each family. To quantitatively analyze the growth performance of these six families, length-specific growth rate (SGR_L) and weight-specific growth rate (SGR_W) were calculated using the following equation:

$$SGR = \frac{\ln(x_2/x_1)}{t_2 - t_1} \times 100$$

In the above equation, x_1 and x_2 represent weight or length obtained at time point t_1 and t_2, respectively. One-way analysis of variance (ANOVA) followed by Tukey's post-hoc test (Systat Software Inc., San Jose, CA) was utilized to identify significant ($p < 0.05$) differences in growth parameters (initial weight or length, final weight or length, SGR_L and SGR_W) among the six PIT-tagged families. In a functional genomic study aimed to

identify transcriptomic differences between families with different growth rates, it is important to select families that show significant differences in SGR_L and SGR_W, while showing no significant differences ($p \geq 0.05$) in both weight and length at the sampling time point. This is because significant differences between families in fish body size at sampling time (for gene expression) may indicate differences in developmental stages that could influence gene expression. Therefore, for microarray- and QPCR-based transcript expression analyses, we selected three triploid families that collectively represented differences in growth performance (two fast-growing families AS11 and AS26 and one slow-growing family AS25) while showing no significant differences in body size at tissue sampling time (t_2). All of the fish in this study were cultured at AquaBounty's hatchery facility (Fortune, Souris, PE). Technicians from the facility collected the growth data and conducted tissue sampling. All of the data and crude RNA samples were sent to Ocean Sciences Centre for further data analysis and later functional genomics studies.

2.2 Detection of the GH transgene and confirmation of triploidization

To assess for the presence of the integrated GH transgene, polymerase chain reactions (PCRs) were performed by personnel at the AquaBounty facility according to standard operating procedures developed by AquaBounty Canada.

Ploidy of each individual was determined by personnel at the AquaBounty facility using flow cytotometry on a Becton Dickinson (BD) FACSCalibur flow cytometer. Instrument quality control for DNA quantitation was performed using CellQuest Pro

software and DNA QC particles (BD #349523) to assess resolution and linearity. For each individual, two drops of heparinized blood from a syringe were mixed with 500 µl of sheath fluid (Biosure #1019). Eighty µl of the blood-sheath fluid mixture were mixed with 500 µl of propidium iodide (PI) solution (Biosure #1021) along with 40 µl of chicken red blood cells (Biosure #1005) as an internal staining control. Samples were incubated in PI solution in the dark for 10 min prior to analysis. The determination of ploidy for individual blood samples was performed through comparison with diploid control samples (animals not subjected to pressure shock) prepared in the manner described above. When the mean peak channel of fluorescence for the pressure-shocked treated sample fell to within 10% of the mean peak channel of the diploid control, the sample was scored as diploid. If the mean peak channel of the treated sample fell within 10% of a 1.5 times multiple of that of the diploid control, the sample was scored as triploid. Ten thousand events were collected for each sample analyzed. Any individuals lacking the GH transgene and/or having unanticipated ploidy were removed from the study.

2.3 Liver tissue sampling and RNA preparation

At the sampling time point, fish were euthanized using a sharp blow to the head. The liver tissues harvested from each individual using standard molecular biology aseptic techniques were immediately flash-frozen in liquid nitrogen and stored at -70°C until use. Total RNA was extracted using the TRIzol reagent (Invitrogen, Burlington, ON) following the manufacturer's instructions. Personnel in AquaBounty facility performed

the liver tissue sampling and TRIzol RNA extraction. However, due to unsuccessful column-purification of TRIzol-prepared RNA samples (i.e. failure of RNA to bind to the column), the RNA was re-extracted using a phenol-chloroform method. The TRIzol-prepared RNA was firstly separated from organic materials by centrifugation with an equal volume of 50% Tris-buffered phenol (pH=8; Sigma-Aldrich, St. Louis, MO), 48% chloroform (Sigma-Aldrich), and 2% isoamyl alcohol (Fisher Scientific, Whitby, ON) (25: 24: 1) mixture at 20817×g at 4°C for 20 min. The RNA was then recovered from the aqueous layer from the previous step by precipitating in 0.1 volume of 3M sodium acetate (pH5.2; Ambion, Burlington, ON) and 2.2 volumes of 95% ethanol (Greenfield, Toronto, ON) at -80°C for an hour, followed by centrifugation at 20817×g at 4°C for 30 min. The resulting RNA pellet was washed in five volumes of 70% ethanol by centrifugation at 20817×g at 4°C for 20 min, air-dried at room temperature for 5-10 min, and dissolved in 0.3 volume of nuclease-free water.

To degrade any residual genomic DNA, the individual total RNA samples were treated with 6.8 Kunitz units DNase-I (RNase-Free DNase Set, QIAGEN Inc., Mississauga, ON) at room temperature for 10 min, followed by column purification using RNeasy Mini kit (QIAGEN) following the manufacturer's instructions. The quantity and quality of cleaned RNA samples were assessed by Nanodrop (Thermo Fisher Scientific, Waltham, MA) spectrophotometry and 1% agarose gel electrophoresis, respectively. The quality of RNA samples was also calculated using a 2100 BioAnalyzer (Agilent Technologies, Mississauga, ON) and associated RNA 6000 Nano and Pico LabChip kits following the manufacturer's protocols.

2.4 Microarray experimental design and procedures

The 32K cGRASP cDNA microarray platform (Koop et al., 2008) (http://web.uvic.ca/grasp/microarray/array.html) was utilized in this study to identify changes in transcript expression associated with growth rate in 3NGHTg Atlantic salmon. The microarray study was comprised of two independent direct comparisons of 4 replicate microarrays including two dye-swaps (a total of 8 slides) using three 3NGHTg families of Atlantic salmon with varying growth rate. These comparisons were used to identify reproducibly differentially expressed hepatic transcripts between fast-growing salmon families (AS11 and AS26) and a slow-growing salmon family (AS25).

The microarray target syntheses and hybridizations were performed using the 3DNA Array900 kit (Genisphere, Hatfield, PA) following the manufacturer's instructions with minor modifications. Briefly, 1 μg of pooled RNA containing equal contribution of individuals ($n \geq 6$) from one family was reverse transcribed in a DNA Engine Tetrad 2 Peltier thermal cycler (Bio-Rad Laboratories, Hertfordshire, England, UK) at 42°C with a heated lid for 2.5 hours in a final volume of 10.5 μl containing Superscript II (10 U μl^{-1}, Invitrogen), unlabeled dNTPs (0.5 mM), 1X SuperScript II first strand buffer, 0.01 M DTT, and Oligo(dT) RT primers (0.1 pmole μl^{-1}) with anchored Cy3 or Cy5 capture sequences. The reactions were terminated by incubating samples with 2 μl of 0.5 M NaOH/50 mM EDTA (Ambion) in the thermal cycler at 65°C with a heated lid for 10 min and subsequently neutralized with 2.4 μl of 1M Tris-HCl (pH=7.5). Prior to hybridization, microarrays (printing batch JL002) were washed twice for 10 min in 0.1% SDS (Ambion) and 5 times for 1 min in nuclease-free water (Fisher Scientific) with

gentle agitation at room temperature and then dried by centrifugation in 50 ml conical tubes (BD Scientific, Mississauga, ON) for 5 min at 800 rpm at room temperature. The synthesized cDNA samples anchored with Cy3 or Cy5 capture sequences were hybridized to microarrays using LifterSlip hybridization covers (Thermo Fisher Scientific) with pre-warmed (hybridization temperature 50°C) formamide based hybridization buffer and LNA-dT blocker (included in the 3DNA Array900 kit). The microarrays were placed in hybridization chambers (Corning, Lowell, MA) and incubated at 50°C in a covered water-filled plastic container placed inside a hybridization oven for 16 hours. After the first hybridization, LifterSlip covers were floated-off in 0.2% SDS/2X SSC buffer (Ambion) at 50°C and the cDNA-hybridized microarrays were subjected to the following wash steps with gentle agitation at room temperature to remove unbound cDNAs: 0.2% SDS/2X SSC buffer for 15 min, 2X SSC for 15 min, 0.2X SSC for 15 min and 0.2X SSC for 5 min. After washing, microarrays were dried by centrifugation as described above prior to the second hybridization. In the second hybridization, Cy3 and Cy5 capture reagents were hybridized to the microarrays for four hours in hybridization chambers in a covered water-filled plastic container placed inside a hybridization oven at 50°C. The second hybridization and subsequence procedures were conducted under dim light to prevent quenching of the fluorescent dyes. The removal of LifterSlip covers and array wash procedures were repeated as described for the first hybridization.

2.5 Microarray data acquisition and analysis

Tagged image file (TIF) images containing fluorescent data were obtained using a ScanArray GX Plus microarray scanner and ScanArray Express software v4.0 (PerkinElmer, Wellesley, MA) at 10 μm resolution and 90% laser power. Raw fluorescent signal of microarray spots in a given area (e.g. one circle containing approximately four sub-grids) was used to determine signal strength in Cy3 and Cy5 channels of a given microarray. The differences in signal strength between Cy3 and Cy5 channels from a given microarray were balanced through adjustment of photomultiplier tube (PMT) values. As a result, in comparison AS11 vs. AS25, PMTs were set to 70 in Cy5 channel and 80 or 81 in Cy3 channel; in comparison AS26 vs. AS25, PMTs ranged from 54 to 58 in Cy5 channel and from 57 to 61 in Cy3 channel. The fluorescent intensity data was extracted from TIF images using ImaGene v7.5 (BioDiscovery, El Segundo, CA). Background correction and Lowess normalization (BCLN), and identification of reproducibly differentially expressed features between fast-growing and slow-growing families, were performed in GeneSpring GX v7.3 (Agilent Technologies). In order to remove microarray features with fluorescent signal close to background from informative gene lists, thresholds were calculated per channel and per array as the median background signal of all salmonid features in the 32K microarray plus 2 standard deviations. In this microarray study, a feature was only considered informative if it: 1) exhibited more than two-fold difference in BCLN expression between fast-growing and slow-growing 3NGHTg Atlantic salmon families in any three out of four technical replicate microarrays (including at least one dye-swap); 2) showed the same direction of expression change in

the fourth technical replicate; and 3) passed threshold in all four technical replicate microarrays in the dominant channel (the dominant channel in the AS11 > AS25 gene list is AS11, i.e. the higher expressing sample or channel).

The majority of the informative transcripts from the microarray study were re-annotated using the best BLASTx or BLASTn hit (lowest E-value < 10^{-5} with an informative gene name) of the expressed sequence tag (EST) representing a given informative microarray feature. For those microarray feature ESTs with significant (E-value < 10^{-5}) BLASTn hits but no informative gene names, BLASTx alignment was performed on the best BLASTn hits, and the first informative name for the resulting best (lowest E-value < 10^{-5}) BLASTx hits were used to re-annotate these transcripts. To functionally annotate microarray-identified transcripts, best informative BLASTx or BLASTn hits were used to obtain gene ontology (GO) terms from Swiss-Prot Protein Knowledgebase (http://www.uniprot.org) if the GO terms were available. Otherwise, GO terms were gathered using best BLASTx or BLASTn hits (lowest E-value <10^{-5}) from *Homo sapiens*, *Mus musculus* or *Danio rerio* selected from the BLAST results. For a given informative feature, all of the GO terms from the molecular function (MF) category (if available) were selected for gene functional annotation. If GO terms from the MF category were not available, then all of the GO terms from the cellular component (CC) category were used for gene functional annotation. Lastly, if MF or CC category had no available GO terms, then all of the GO terms from the biological process (BP) category were used for functional annotation.

Multiple microarray informative features with same gene name within a given gene list could potentially represent one or more genes (e.g. paralogues). For example,

multiple informative microarray features were BLAST-identified as Glyceraldehyde-3-phosphate dehydrogenase. Therefore, in order to determine if these informative features represented a single gene or multiple paralogues, ESTs representing Atlantic salmon microarray features were used to query the NCBI non-redundant nucleotide database by BLASTn; all same-named Atlantic salmon nucleotide sequences were collected from the list of BLASTn hits. These sequences were then subjected to multiple alignment analysis using the MegAlign function of the Lasergene v8.0 software (DNASTAR Inc., Madison, WI). Based on the similarity between microarray features and these nucleotide sequences obtained from the nr database using BLASTn, a given microarray feature was deemed to represent a NCBI nucleotide sequence if the percent identity was greater than or equal to 95% at the nucleotide level. Otherwise, the microarray feature was considered to be paralogous to a given Atlantic salmon nucleotide sequence.

2.6 Gene ontology analysis

In order to identify the biological processes that were significantly differently represented between gene differentially expressed in 3NGHTg Atlantic salmon families with varying growth performance, the GO enrichment analyses for all hierarchies were carried out for each of the two microarray comparisons using the BLAST2GO suite (Conesa and Gotz, 2008; Conesa et al., 2005; Gotz et al., 2008). Collaborator Charles Y. Feng performed this analysis. All 31,982 salmonid cDNA features from the 32K cGRASP cDNA microarray were re-annotated using the high throughput BLASTx function with E-value cut-off set at 10^{-3}, and only the 20 best BLASTx hits were retained for GO

mapping. The GO mapping and annotation were also carried out using BLAST2GO suite with all parameters at default settings. Using the distribution of GO terms associated with the salmonid cDNA features of the 32K cGRASP cDNA microarray as the reference, Fisher's exact test was used to determine if a given GO term was significantly ($p < 0.05$; ≥ 3 times) associated at a higher frequency with the transcripts of a pooled list of genes that were differentially expressed in a fast-growing vs. slow-growing 3NGHTg Atlantic salmon families microarray comparison.

2.7 QPCR

QPCR studies were conducted using individual liver RNA samples from the three 3NGHTg Atlantic salmon families involved in the microarray experiment. For each RNA sample, template cDNA was synthesized from 1 μg of DNase I-treated and column-purified total RNA using random primers and SuperScript II reverse transcriptase (SuperScript™ II RT) (Invitrogen) following the manufacturer's instructions. Briefly, a mixture of 1 μg total RNA, dNTPs (0.5 mM each), and random primers (12.5 ng μl^{-1}) were incubated in the thermal cycler at 65°C with a heated lid for 5 min and then chilled on ice for 2 min. Following the snap cool, 1X first strand buffer, 0.01M DTT, and SuperScript II reverse transcriptase (10 units μl^{-1}) were added to the mixture and the total 20 μl of reaction was mixed gently by pipette and then incubated in the thermal cycler following the thermal profile (25°C for 10 min, 42°C for 50 min, 70°C for 15 min) with the lid heated. The resulting cDNAs were diluted 1:9 with nuclease-free H_2O (Invitrogen) and stored at -20°C until QPCR amplification.

The QPCR primers for the normalizer and TOIs were designed based on the cDNA sequences representing the selected informative features using the Primer3 program (http://frodo.wi.mit.edu/primer3/) (Rozen and Skaletsky, 2000). Each primer pair was quality-checked before use, which included calculation of amplification efficiency ($E = 10^{[-1/\text{slope}]}$) (Pfaffl, 2001) using five 1:5 serial dilutions of pooled cDNA (starting with cDNA corresponding to 10 ng of input total RNA) with equal contributions by all individuals involved in the QPCR study. For a given primer pair, quality control was performed in triplicates to establish technical replicates. In addition, dissociation (melt) curves were also performed and analyzed to ensure that there was a single peak at the expected melting temperature of the amplicon, and no-template controls (NTCs) were performed to ensure the absence of non-specific amplification. In order to validate microarray results with QPCR, polyadenylate-binding protein 1 (PABP1) was selected as a normalizer because it is stably expressed ($0.9 <$ fold change < 1.4) between fast-growing 3NGHTg Atlantic salmon families (AS11 and AS26) and a slow-growing 3NGHTg Atlantic salmon family (AS25) in 7 out of 8 microarrays (data not shown). To validate PABP1 suitability as a normalizer in this study, QPCR expression analysis using individual cDNA samples was performed in the three 3NGHTg Atlantic salmon families (AS11, AS25 and AS26) and the difference of C_T (cycle threshold) across all tested samples in the same study was within a range of 1.5 cycles.

To quantify mRNA expression levels of TOIs, 13 µl amplification reactions that contained 2 µl of diluted cDNA (representing 10 ng of input total RNA), 50 nM each of forward and reverse primer, and 1X Power SYBR Green PCR Master Mix (Applied

Biosystems, Foster City, CA) were performed on a 7500 Real Time PCR System (Applied Biosystems) with the following cycling conditions: 50°C for 20 s, 95°C for 10 min, and 40 cycles of (95°C for 15 s and 60°C for 1 min) with the fluorescent signal measured at the end of each 60°C step. The fluorescence thresholds and baseline were determined automatically using the 7500 Fast Software Relative Quantification Study Application (Version 2.0; Applied Biosystems). Three TOIs were included in each of the multi-plate studies that consisted of four 96-well format plates. A linker cDNA sample made of equal contribution from randomly selected cDNA samples involved in the QPCR study was run on every plate in triplicate to control for plate variability (C_T value varied less than 0.5 among plates in the same study). In addition, the samples were also randomly distributed among plates in a multi-plate study to further eliminate possible biases as a result of plate variability. For any given sample, the TOIs and normalizer were run in triplicates (technical replicates) on the same plate, and NTCs were performed in each plate to ensure the absence of primer dimers and template contamination. Amplicons for each TOI were run on a 2% agarose gel stained with ethidium bromide alongside a 100 bp DNA ladder (Invitrogen) to confirm the correct sizes of amplified products.

The relative quantity (RQ) of each QPCR target transcript for every studied individual was calculated in the 7500 Real Time PCR System using the $2^{-\Delta\Delta CT}$ quantification method including the calculated amplification efficiencies for TOIs and the normalizer (Livak and Schmittgen, 2001). The RQ values for each target for each sample were calibrated to the individual with the lowest normalized expression for a given TOI. To determine if there were significant ($p < 0.05$) differences in transcript expression

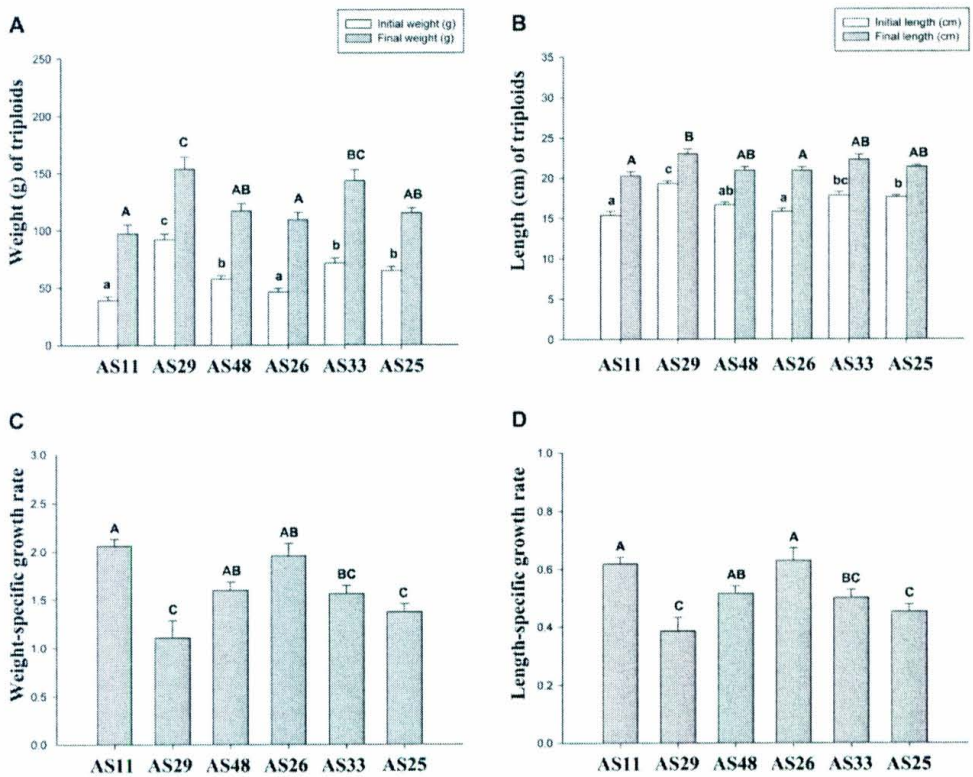
between fast-growing and slow-growing families, two-sample t-tests were performed on RQ values using Minitab v15.1 (Minitab Inc., State College, PA.).

3. RESULTS

3.1 Growth performance of 3NGHTg Atlantic salmon

Growth performance of the experimental 3NGHTg Atlantic salmon families was calculated over a period of approximately 45 days. Three families with larger body size (AS29, AS33 and AS25) and three families with smaller body size (AS11, AS48 and AS26) were selected from 19 experimental families based on their weight and length measurements (data not shown). The six families were PIT tagged and subjected to growth rate evaluation (Fig. 1). At the initial time point (t_1) in the growth study, the weight of family AS29 (mean 92.1 g) was significantly ($p < 0.05$) higher than that of families AS33 (mean 71.3 g), AS25 (mean 64.5 g), and AS48 (mean 57.3 g); families AS11 (mean 39.1 g) and AS26 (mean 46.1 g) had smaller initial body weights, and these were significantly lower than the initial body weights of the other four experimental families (Fig. 1A). At the final time point (t_2; when samples were taken for gene expression analyses), no significant differences were observed in either weight or length in families AS11, AS48, AS26, and AS25 (Fig. 1B); the final weight of AS29 was significantly higher than the final weight of AS11, AS48, AS26, and AS25, and the final length of AS29 was significantly higher than the final lengths of AS11 and AS26 (Fig. 1 A and B). In terms of specific growth rate during the period of approximately 45 days, both SGR_W and SGR_L for families AS11, AS48, and AS26 were significantly higher than family AS25, and no significant differences ($p \geq 0.05$) were detected in growth rate among families AS11, AS48, and AS26 (Fig. 1 C and D). Therefore, family AS11,

Fig. 1. Growth performance data of six PIT-tagged 3NGHTg Atlantic salmon families (AS11, AS29, AS48, AS26, AS33, and AS25) during a period of approximately 45 days. A. Initial and final weight (g); B. Initial and final length (cm); C. Weight-specific growth rate (SGR_W); D. Length-specific growth rate (SGR_L). All data are presented as means (± SEM). For all growth parameters presented in panel A-D, different letters identify significant ($p < 0.05$) differences among the six families enrolled in this study. In panels A and B, significant differences in both initial weight and length among families were identified by different lower case letters, and significant differences in both final weight and length among families were identified by different upper case letters. In panels C and D, significant differences in SGR_W and SGR_L among families were identified by different upper case letters. See Section 2.1 for calculations of SGR and significance.


A
Initial weight (g)
Final weight (g)
Weight (g) of triploids
250
200
150
100
50
0
a
A
c
C
b
AB
a
A
b
BC
b
AB
AS11 AS29 AS48 AS26 AS33 AS25
B
Initial length (cm)
Final length (cm)
Length (cm) of triploids
35
30
25
20
15
10
5
0
a
A
c
B
ab
AB
a
A
bc
AB
b
AB
AS11 AS29 AS48 AS26 AS33 AS25
C
Weight-specific growth rate
3.0
2.5
2.0
1.5
1.0
0.5
0.0
A
C
AB
AB
BC
C
AS11 AS29 AS48 AS26 AS33 AS25
D
Length-specific growth rate
1.0
0.8
0.6
0.4
0.2
0.0
A
C
AB
A
BC
C
AS11 AS29 AS48 AS26 AS33 AS25

AS25, and AS26 were selected for the functional genomic study based on the following two criteria: 1) the absence of any differences in either final weight or length among these families reduces the possibility of comparing families at different developmental stages); and 2) the presence of significant differences in both SGR_W and SGR_L among these families, with AS11 and AS26 having the highest and second highest SGR_W and SGR_L and AS25 having the second lowest SGR_W and SGR_L (enabling comparisons between fast-growing and slow-growing families) (Fig. 2; see Appendix I for complete data).

3.2 RNA quality control

We sampled liver tissue from nine individual fish from each family for RNA-based studies (ten fish were sampled for family AS26, see Section 2.1 for details). However, one individual from family AS11 was determined to be non-transgenic and it was excluded from the study (data not shown; see Section 2.2 for transgene detection).

The quality of RNA samples used in the microarray and QPCR studies were checked using a Nanodrop spectrophotometer and gel electrophoresis. The optical density (OD) 260/280 and 260/230 ratios were used to determine the purity of RNA samples as nucleic acids have highest ultraviolet light absorption at 260 nm. The 260/280 ratio of RNA samples contributing to microarray and QPCR studies ranged from 1.92 to 2.17, indicating no or very low protein contaminants in these samples, and the 260/230 ratio ranged from 1.83 to 2.39, indicating no or very low detectable solvents, salt and other contaminants in these samples (Table 1). Ethidium bromide stained 1% agarose gel electrophoresis was performed on RNA samples involved in the study to check RNA

Fig. 2. Growth performance data of three PIT-tagged 3NGHTg Atlantic salmon families (AS25, AS11, and AS26) during a period of approximately 45 days. A. Initial and final weight (g); B. Initial and final length (cm); C. Weight-specific growth rate (SGR_W); D. Length-specific growth rate (SGR_L). All data are presented as means (± SEM), and the complete growth data on all individuals are listed in Appendix I. For all growth parameters presented in panels A-D, different letters identify significant ($p < 0.05$) differences between the three families enrolled in this study. In panels A and B, significant differences in both initial weight and length among families were identified by different lower case letters, and significant differences in both final weight and length among families were identified by different upper case letters. In panels C and D, significant differences in SGR_W and SGR_L among families were identified by different upper case letters. These three families were selected from the six PIT-tagged 3NGHTg Atlantic salmon families based on their comparable sizes at sampling point (i.e. no significant differences ($p \geq 0.05$) in final weight and length) and significantly different specific growth rates (i.e. significantly differences ($p < 0.05$) in SGR_W and SGR_L over approximately 45 days). See Section 2.1 for additional information on the selection of families for the gene expression analyses. The growth performance of the six PIT-tagged families is shown in Fig. 1.

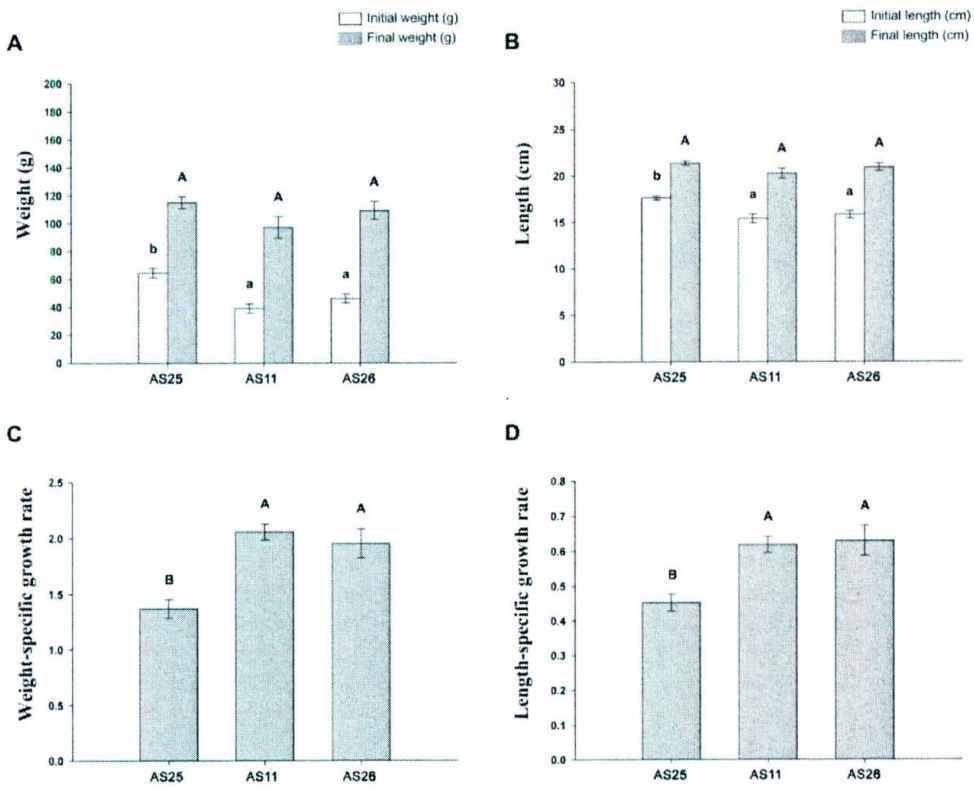

A
Initial weight (g)
Final weight (g)
Weight (g)
200
180
160
140
120
100
80
60
40
20
0
b
A
a
A
a
A
AS25
AS11
AS26
B
Initial length (cm)
Final length (cm)
Length (cm)
30
25
20
15
10
5
0
b
A
a
A
a
A
AS25
AS11
AS26
C
Weight-specific growth rate
2.5
2.0
1.5
1.0
0.5
0.0
B
A
A
AS25
AS11
AS26
D
Length-specific growth rate
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
B
A
A
AS25
AS11
AS26

Table 1. Quality of purified liver RNA samples from triploid GH transgenic (3NGHTg) Atlantic salmon families AS11, AS25 and AS26.

Sample[1]	Nanodrop[2]		Bioanalyzer RIN[3]	QPCR normalizer C_T by multi-plate study[4]					
	260/280	260/230		1	2	3	4	5	6
AS11 (n=8)									
151-F	2.17	2.27	6.8	19.3	21.6	21.7	21.4	21.1	22.0
155-F	2.13	2.33	8.8	19.1	21.5	20.8	20.3	20.0	21.3
156-M	2.15	2.34	9.2	18.8	21.2	20.8	20.4	20.1	20.9
160-F	2.13	2.34	8.0	19.5	21.4	21.4	20.7	20.5	21.3
161-M	2.11	2.12	9.6	19.3	21.2	21.6	21.0	20.8	21.1
162-F	2.14	1.90	9.6	18.9	21.0	20.9	20.5	20.2	21.4
166-M	2.12	2.39	8.1	19.4	21.2	21.0	21.0	20.7	21.5
168-M*	2.19	2.08	8.2	N/A	N/A	N/A	N/A	N/A	N/A
AS25 (n=9)									
153-F	2.08	2.17	6.9	N/A	N/A	N/A	N/A	N/A	N/A
154-F	2.10	2.35	7.3	19.5	21.9	21.5	21.1	20.9	21.7
155-F	2.03	2.28	8.3	19.2	21.6	20.9	20.4	20.1	21.2
156-M*	2.05	1.83	6.3	19.8	21.9	21.7	21.0	20.9	21.9
157-M	2.14	2.34	7.7	19.2	21.1	21.5	21.4	21.2	22.0
159-F	2.14	2.32	7.6	19.3	21.3	21.0	20.7	20.4	21.2
160-M	2.14	2.29	5.3	19.6	21.1	21.6	21.0	20.8	21.7
164-F*	1.92	2.25	5.8	19.3	21.3	21.1	20.7	20.5	21.2
167-F*	2.04	1.89	5.9	19.4	21.1	21.0	20.8	20.5	21.7
AS26 (n=10)									
252-F	2.15	2.33	8.3	N/A	N/A	N/A	N/A	N/A	N/A
253-F*	2.06	2.34	N/A	18.9	21.6	21.0	20.6	20.3	21.0

254-F	2.17	2.30	8.9	18.9	21.4	21.0	20.6	20.4	20.9
256-M	2.16	2.36	9.1	18.9	21.3	21.0	20.6	20.0	20.9
257-F	2.16	2.37	9.1	18.9	20.7	21.0	20.5	20.2	21.0
260-M	2.06	2.11	8.5	18.9	20.7	20.8	20.1	20.1	20.7
261-M	2.07	2.34	7.2	19.3	21.1	21.5	20.7	20.2	21.1
263-F	2.15	2.26	7.6	19.0	20.9	21.0	20.3	20.1	20.9
264-F*	2.15	2.34	8.0	N/A	N/A	N/A	N/A	N/A	N/A
265-F*	2.17	2.33	6.7	18.9	20.8	21.1	20.4	20.2	21.0

[1]Samples are ethanol-precipitated, DNase treated, and column-purified liver RNA samples. RNA samples of insufficient quantity (indicated with an asterisk) were excluded from the microarray study. The remainder of the samples contributed equally to the formation of RNA pools that were used in microarray studies (AS11 vs. AS25 and AS26 vs. AS25). "F" indicates RNA samples that were extracted from female 3NGHTg Atlantic salmon, and "M" indicates RNA samples that were extracted from male 3NGHTg Atlantic salmon.

[2]Optical density (OD) 260/280 ratio, and OD 260/230 ratios were taken using a NanoDrop ND-1000 spectrophotometer.

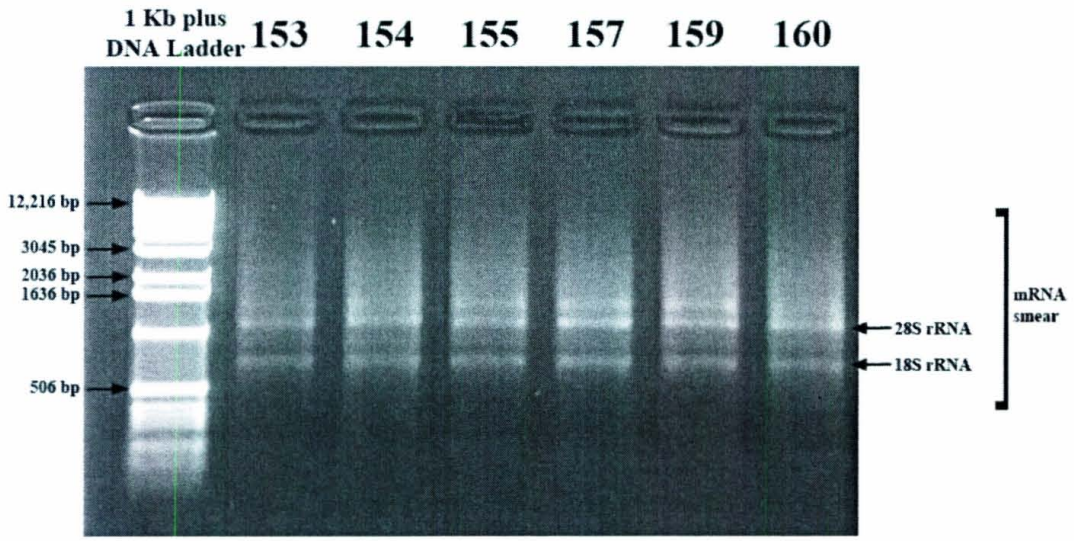
[3]RNA quality was evaluated using an Agilent 2100 Bioanalyzer and associated RNA 6000 Nano and Pico LabChip kits. RNA integrity numbers (RINs) were calculated by Agilent2100 Expert software with a range of 1 to 10, with 1 being the most degraded profile and 10 being the most intact. The Bioanalyzer was unable to determine RIN for sample AS26_3N_253_F possibly due to the presence of RNA secondary structure.

[4]The target transcripts involved in each of the multi-plate studies are as follows: study 1: APOA1, APOA2, D5DP; study 2: B2M1, B2M2, SEPP1; study 3: NUPR1, FTM, AA5; study 4: GADPH1, GADPH2, ACBP; study 5: APOAIV, SEPP2; study 6: ADAMTS-1. N/A denotes samples that were not included in this QPCR study due to outlier normalizer C_T values (i.e. AS25: 153-F) in a separate QPCR study on the impact of triploidization on hepatic gene expression (see Section 1.5) or insufficient RNA quantity (i.e. AS11: 168-M; AS26: 252-F, 264-F).

quality. A gel image of electrophoretically separated purified RNA samples from 3NGHTg family AS25 is shown as an example (Fig. 3). The image shows that the RNA samples were of high quality; the agarose gel image showed the presence of visible 18S and 28S rRNA bands and mRNA (smear in the background), and the absence of a high molecular weight genomic DNA in these samples (Fig. 3). The RNA integrity numbers (RINs) calculated by Agilent2100 Expert software are within a range of 1 to 10, with 1 being the most degraded profile and 10 being the most intact. RIN number of the tested samples varied from 5.3 to 9.6 (Table 1). There was no observed correlation between RIN values and normalizer C_T values, suggesting that all RNA samples involved in this work were of acceptable quality for microarray and QPCR studies.

For each family, equal amounts of DNase-treated, column-cleaned total RNA samples contributed to a pool (AS11 pool: n=7; AS25 pool: n=6; AS26 pool: n=7) for microarray study. One individual from family AS11 and three individuals from each of families AS25 and AS26 were excluded from the microarray study due to insufficient RNA quantity (Table 1). For the QPCR study, one individual from AS25 (153-F) was removed from the study due to outlier normalizer C_T values, where outlier was defined as C_T that differ by more than 1.5 cycles from others in the same study; one individual from AS11 and two individuals from AS26 were removed from QPCR study due to insufficient RNA quantity (Table 1).

Fig. 3. Image of an ethidium bromide stained 1% agarose gel showing electrophoretically separated, DNase-treated purified liver RNA samples (n=6) from triploid GH transgenic (3NGHTg) Atlantic salmon family AS25. The 1Kb plus DNA ladder (Invitrogen) was electrophoretically separated in lane 1. The numbers above lanes 2 through 7 represent fish individuals from family AS25 that contributed liver RNA to the microarray study (see Table 1 for RNA quality). The visible bands in lanes 2 through 7 indicate the presence of 18S and 28S ribosomal RNA (rRNA), and the background smear in these lanes indicates the presence of messenger RNA (mRNA). No visible band of high molecular weight near the wells of lanes 2 through 7 indicates the absence of genomic DNA in these RNA samples.

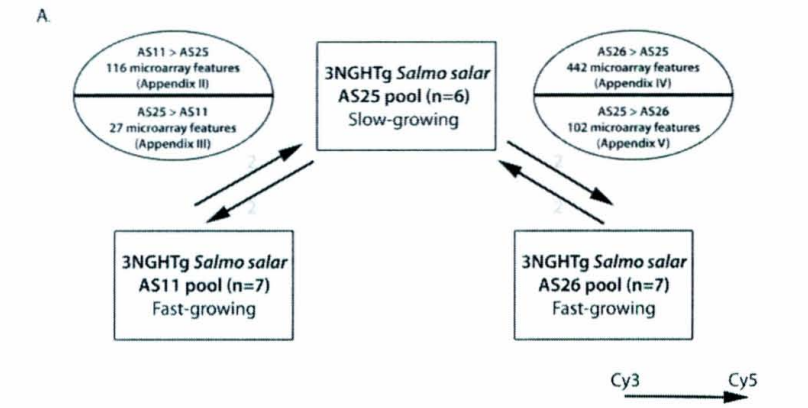

1 Kb plus
DNA Ladder
153
154
155
157
159
160
12,216 bp
3045 bp
2036 bp
1636 bp
506 bp
28S rRNA
18S rRNA
mRNA
smear

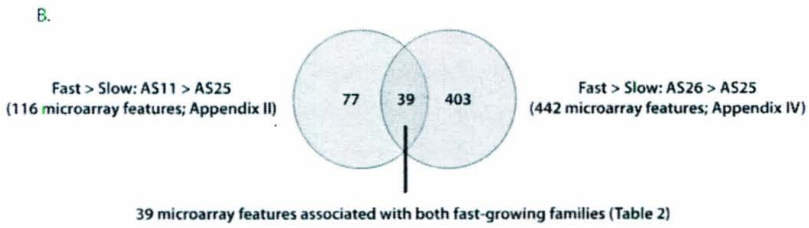
3.3 Family-specific differences in hepatic transcript expression

To identify differences in gene transcription that are associated with enhanced growth performance in 3NGHTg Atlantic salmon families, I compared two fast-growing families (AS11 and AS26) with one slow-growing family (AS25) using the 32K cGRASP cDNA microarray platform (Fig. 4A). In total, the microarray study identified 143 differentially expressed features (116 more highly expressed in AS11 and 27 more highly expressed in AS25) in the comparison of AS11 and AS25 pools, and 544 differentially expressed features (442 more highly expressed in AS26 and 102 more highly expressed in AS25) in the comparison of AS26 and AS25 pools (Fig. 4A). All informative microarray features are shown in Appendices (i.e. AS11 vs. AS25: Appendices II and III; AS26 vs. AS25: Appendices IV and V) along with identification information of best BLASTx or BLASTn hit from NCBI and cGRASP databases and associated GO terms from Swiss-Prot Protein Knowledgebase (see Section 2.5 for details).

In order to identify putative growth-relevant transcripts that were reproducibly expressed at a higher level in fast-growing families, informative features with higher expression level in AS11 (116 features; Appendix II) and AS26 (442 features; Appendix IV) were compared using Venn diagrams with GeneSpring software. The intersection of these gene lists consisted of 39 informative microarray features that were consistently expressed at a higher level in fast-growing families (AS11 and AS26) compared to the slow-growing family (AS25) (Fig. 4B; Table 2). Within the list of 39 potential enhanced growth-associated microarray features, four features had BLAST identification and

Fig. 4. Microarray study to identify differentially expressed hepatic transcripts between two fast-growing 3NGHTg Atlantic salmon families (AS11 and AS26) and a slow-growing 3NGHTg family (AS25). A. Microarray experimental design and results summary. Within each comparison, microarray features were considered informative if they: 1) presented more than two-fold higher background-corrected, Lowess-normalized (BCLN) expression in a given comparison (AS11 vs. AS25 or AS26 vs. AS25) in any three arrays (including at least one dye-swap) out of four technical replicate arrays; 2) showed the same direction of expression change in the fourth array; and 3) passed threshold in all four technical replicate microarrays. See Section 2.5 for details on microarray data analysis, and Appendices II-V for complete gene lists. The base of each arrow represents the Cy3-labeled target, and the head of each arrow represents the Cy5-labeled target. B. Venn diagram analysis was used to identify the putative growth-relevant features (listed in Table 2) that were consistently expressed at a higher level in the two fast-growing families relative to the slow-growing family. C. Venn diagram analysis was used to identify the putative growth-relevant transcript (listed in Table 2) that was consistently expressed at a higher level in the slow-growing family compared to the two fast-growing families.


A.
AS11 > AS25
116 microarray features
(Appendix II)
AS25 > AS11
27 microarray features
(Appendix III)
3NGHTg Salmo salar
AS25 pool (n=6)
Slow-growing
AS26 > AS25
442 microarray features
(Appendix IV)
AS25 > AS26
102 microarray features
(Appendix V)
3NGHTg Salmo salar
AS11 pool (n=7)
Fast-growing
3NGHTg Salmo salar
AS26 pool (n=7)
Fast-growing
Cy3
Cy5


B.
Fast > Slow: AS11 > AS25
(116 microarray features; Appendix II)
77
39
403
Fast > Slow: AS26 > AS25
(442 microarray features; Appendix IV)
39 microarray features associated with both fast-growing families (Table 2)

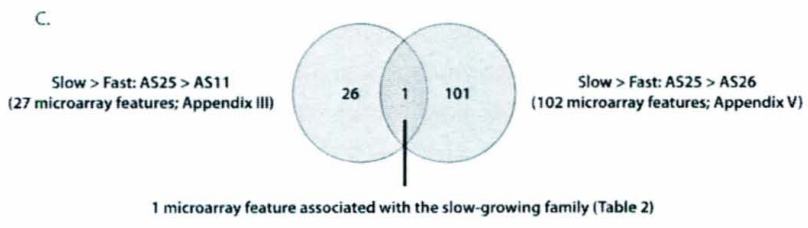

C.
Slow > Fast: AS25 > AS11
(27 microarray features; Appendix III)
26
1
101
Slow > Fast: AS25 > AS26
(102 microarray features; Appendix V)
1 microarray feature associated with the slow-growing family (Table 2)

Table 2. Forty microarray features identified in both microarray comparisons between fast-growing 3NGHTg Atlantic salmon families (AS11 and AS26) and a slow-growing 3NGHTg family (AS25).

EST [1] (Microarray features)	Best BLASTX or BLASTN [(N)] Hit [2]			Functional Annotation (Gene Ontology) of Best BLASTX or BLASTN [(N)] Hit [3]	Microarray Mean Fold Change (SEM)[4]		QPCR Overall Fold Change[5]	
	Gene Name	Length (% identity)	E-value					
Expressed at higher levels in fast-growing families (AS11 and AS26)					**AS11>AS25**	**AS26>AS25**	**AS11>AS25**	**AS26>AS25**
Carbohydrate metabolism								
CA042530	6-phosphofructokinase, liver type [AAI26579; *Bos taurus*]	199 (78%)	9E-87	6-phosphofructokinase activity; ATP binding; Metal ion binding (GO:0003872; GO:0005524; GO:0046872) [A1A4J1]	2.87 (0.54)	2.54 (0.55)		
CB492813	Glyceraldehyde-3-phosphate dehydrogenase [ACI33883; *Salmo salar*] (GAPDH *Oncorhynchus mykiss* type 1)	113 (100%)	5E-54	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X3K2]	3.56 (0.76)	17.51 (6.50)		
CB498361	Glyceraldehyde-3-phosphate dehydrogenase [ACI66269; *Salmo salar*] (GAPDH *Oncorhynchus mykiss* type 2)	146 (99%)	5E-78	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X5Z9]	2.31 (0.25)	4.95 (1.83)		
BU965756	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*] (*Salmo salar* type 2)	116 (100%)	5E-60	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	3.57 (0.61)	26.56 (14.65)	*5.0	*3.5

	(GAPDH2, Fig. 13B)			(GO:0051287; GO:0004365) [B5XG76]				
Lipid metabolism								
CB493696	Acyl-CoA-binding protein [ACI68322; *Salmo salar*] (ACBP, Fig. 11A)	42 (95%)	9E-16	Fatty-acyl-CoA binding (GO:0000062) [B5XBV2]	3.02 (0.59)	6.18 (1.69)	1.4	1.7
CA041892	Apolipoprotein A-I precursor [ACI68193; *Salmo salar*] (APOAI *Salmo salar* type 2) (Fig. 12B)	44 (100%)	5E-16	Lipid binding (GO:0008289) [B5XBH3]	3.44 (0.71)	92.40 (54.15)	1.3	*2.0
CB493958	Apolipoprotein A-IV precursor [ACI67266; *Salmo salar*] (APOAIV, Fig. 11B)	121 (98%)	3E-57	Lipid binding (GO:0008289) [B5X8U6]	2.51 (0.38)	4.56 (0.96)	3.7	*5.1
CB493595	Delta5-desaturase-like protein [ABU87822; *Oncorhynchus masou*] (D5DP, Fig. 11C)	87 (99%)	2E-45	Heme binding; Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [A7XUS7]	3.68 (0.62)	3.25 (0.36)	2.7	*5.9
CB497206	Myelin basic protein [AAW52552; *Danio rerio*]/[EZ764180; *Oncorhynchus mykiss*] [(B)]	89 (44%)/44 (100%)	1E-05/ 4E-12	Structural constituent of myelin sheath (GO:0019911) [Q5I2C7]	3.43 (1.04)	16.94 (11.59)		
Protein metabolism								
CA042535	40 kDa peptidyl-prolyl cis-trans isomerase [ACO07506; *Oncorhynchus mykiss*]	103 (100%)	7E-47	Binding; Peptidyl-prolyl cis-trans isomerase activity (GO:0005488; GO:0003755) [C1BEQ3]	2.28 (0.21)	11.14 (3.08)		
CB492405	40S ribosomal protein S11	105 (100%)	3E-54	Structural constituent of ribosome	2.78 (0.15)	10.16 (0.69)		

	[ACO15454; *Caligus clemensi*]			(GO:0003735) [C1C2F1]		
CB491393	40S ribosomal protein S13 [ACO08029; *Oncorhynchus mykiss*]	139 (99%)	9E-73	Structural constituent of ribosome (GO:0003735) [C1BG76]	2.90 (0.31)	71.86 (34.01)
CB492978	40S ribosomal protein S27 [ABJ98653; *Psetta maxima*]	87 (98%)	1E-37	Metal ion binding; Structural constituent of ribosome (GO:0046872; GO:0003735) [A0EZY9]	2.25 (0.27)	4.09 (0.91)
CA060826	Elongation factor 1-alpha 1 [ACN11490; *Salmo salar*]	38 (100%)	2E-11	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	5.22 (1.32)	57.40 (37.08)
CA053189	Glutamate dehydrogenase 1, mitochondrial precursor [BT044837; *Salmo salar*] [N]	515 (100%)	0	Binding; Oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor (GO:0005488; GO:0016639) [B5X1B8]	2.60 (0.56)	2.29 (0.25)
CX245969	Tryptophan 2,3-dioxygenase [AAI51921; *Danio rerio*]	238 (83%)	2E-103	Iron ion binding; Tryptophan 2,3-dioxygenase activity (GO:0005506; GO:0004833) [A7MBU6]	2.57 (0.35)	3.63 (0.55)
Iron homeostasis						
CB493178	Ferritin-H subunit [AAK08117|AF338763; *Oncorhynchus nerka*]	65 (95%)	8E-57	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [Q98TT0]	2.71 (0.63)	5.34 (1.19)
CB487639	Ferritin, middle subunit [ACI66713;	130 (95%)	1E-66	Ferric iron binding;	2.47 (0.47)	17.89 (2.53)

	Salmo salar] (*Oncorhynchus mykiss* type 1)			Oxidoreductase activity (GO:0008199; GO:0016491) [B5X793]				
CB503780	Ferritin, middle subunit [ACI68639; *Salmo salar*] (*Salmo salar* feature)	162 (100%)	4E-89	Ferric iron binding (GO:0008199) [B5XCR9]	2.15 (0.26)	4.35 (0.82)		
CB510731	Ferritin, middle subunit [ACO07744; *Oncorhynchus mykiss*] (*Salmo salar* feature) (Fig. 11D)	124 (100%)	3E-66	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [C1BFE1]	2.18 (0.37)	2.51 (0.43)	*2.1	*3.2
CB497564	Hemoglobin subunit alpha [ACI69100; *Salmo salar*]	143 (99%)	9E-74	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XE30]	3.09 (0.65)	4.32 (1.23)		
CB498419	Hemoglobin subunit alpha-1 [ACO07570; *Oncorhynchus mykiss*]	143 (100%)	8E-76	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [Q98974]	2.57 (0.42)	4.06 (0.47)		
CB497309	Hemoglobin subunit beta-4 [ACO07576; *Oncorhynchus mykiss*]	148 (100%)	6E-80	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BEX3]	3.38 (0.80)	4.08 (0.67)		
Immune- or stress-related responses								
CB505594	Beta-2 microglobulin [AF180486; *Salmo salar*] [N] (*Salmo salar* type 1) (B2M1, Fig. 14A)	799 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DG62] [c]	2.25 (0.26)	3.59 (0.42)	*2.2	*4.0
CA043324	Beta-2-microglobulin precursor [BT047559; *Salmo salar*] [N] (*Salmo*	542 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DD81] [c]	3.00 (0.49)	27.44 (12.89)	*10.5	*8.5

	salar type 2) (B2M2, Fig. 14B)							
CB493926	Keratin 18, simple type I keratin [CAA74664; *Oncorhynchus mykiss*]	73 (100%)	5E-24	Structural molecule activity (GO:0005198) [O57607]	3.05 (0.68)	7.35 (2.66)		
CA048859	MHC Class I (Sasa-UBA) [EF210363; *Salmo salar*] [(N)]	566 (99%)	0	MHC class I protein complex (GO:0042612) [A7KDZ8] [c]	2.55 (0.38)	2.62 (0.28)		
CB490586	Nuclear protein 1 [AAH02109; *Mus musculus*] [(X)] (NUPR1, Fig. 11E)	57 (56%)	4E-11	Nucleus (GO:0005634) [Q9WTK0] [c]	4.60 (1.08)	185.55 (50.85)	1.0	2.2
CA044554	Prothymosin, alpha a [AAH68334; *Danio rerio*] [(X)]	36 (89%)	4E-08	Nucleus (GO:0005634) [Q6NV32] [c]	2.27 (0.11)	22.77 (15.16)		
EG910863	Serum albumin 2 [CAA43187; *Salmo salar*]	232 (78%)	1E-96	Lipid binding; Metal ion binding (GO:0008289; GO:0046872) [Q03156]	4.33 (1.17)	5.71 (0.93)		
Others								
CB496981	DNA-directed RNA polymerases I, II, and III subunit RPABC2 [ACO13758; *Esox lucius*]	56 (98%)	4E-24	DNA binding; DNA-directed RNA polymerase activity (GO:0003677; GO:0003899) [C1BXK5]	1.94 (0.24)	4.33 (1.07)		
CB497579	Glutathione S-transferase [BAA76974; *Oncorhynchus nerka*]	159 (97%)	3E-84	Glutathione transferase activity (GO:0004364) [Q9W647]	2.46 (0.28)	10.76 (2.24)		
CB497659	Heparin cofactor II [AAN71003|AF515273; *Danio rerio*]/[EZ764595; *Oncorhynchus mykiss*] [(B) (X)]	304 (80%)/571 (99%)	1E-174/0	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q8AYE2]	3.03 (0.70)	9.87 (3.18)		
CB498181	Kelch repeat and BTB (POZ) domain containing 10 [ACH70794; *Salmo salar*]	76 (96%)	5E-35	Unknown	2.34 (0.05)	4.02 (1.00)		

CB496780	Kif1-binding protein [ABW89743; *Danio rerio*]	67 (73%)	2E-10	Binding (GO:0005488) [A8WE67]	2.71 (0.42)	6.08 (0.71)		
CB509563	Pre-mRNA-splicing factor 18 [ACO09138; Osmerus mordax]/[EZ871571; *Oncorhynchus mykiss*] [(B)]	247 (55%)/513 (88%)	3E-86/3E-161	Spliceosomal complex (GO:0005681) [C1BJD5] [c]	2.63 (0.50)	7.66 (2.72)		
CA038814	Reverse transcriptase [AAS83200; *Fundulus heteroclitus*]	115 (29%)	1E-08	RNA binding; RNA-directed DNA polymerase activity (GO:0003723; GO:0003964) [Q64IX6]	6.34 (1.42)	3.88 (0.54)		
CA038301	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*]	76 (89%)	2E-30	Unknown	3.89 (1.07)	8.45 (1.61)		
CA044829	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.34 (0.36)	33.33 (19.59)		
Expressed at a higher level in the slow-growing family (AS25)					**AS25>AS11**	**AS25>AS26**	**AS25>AS11**	**AS25>AS26**
CK990279	ADAMTS-1 protein [BAE16358; *Oryzias latipes*] (ADAMTS1, Fig. 11F)	148 (72%)	1E-58	Metalloendopeptidase activity; Zinc ion binding (GO:0004222; GO:0008270) [Q4AED3]	2.68 (0.53)	12.32 (8.84)	1.8	*2.4

[1]Expressed sequence tags (ESTs) were identified by gene name of best BLASTX or BLASTN hit (lowest E-value; E-value < 1e-05) from GenBank nucleotide or protein database.

[2] The length of aligned region, percent identity over aligned region and associated E-value are presented.

[(N)]Indicates best BLASTN hit with an informative gene name;

[(B)]Indicates BLASTX result of the best BLASTN hit from NCBI if the best BLASTN hit was not informative, and is presented in "gene name [BLASTX result]/[BLASTN result]" format;

[(G)]Indicates BLAST result from cGRASP (http://web.uvic.ca/grasp) EST database;

[(X)]Indicates best BLASTX hit from *Homo sapiens*, *Mus musculus* or *Danio rerio*, which was only listed if functional annotations (GO terms) of best BLASTX hit were not available.

Features with same-named BLAST results were analyzed in the MegAlign software and manually assigned as "*Salmo salar* type #" (if more than one paralogous sequence was identified; similarities < 95%) or "*Salmo salar* feature " (if sequence similarity ≥ 95%). The same rules were applied to *Oncorhynchus mykiss* features. The figure numbers are in parentheses for transcripts that were studied using QPCR.

[3]Function of the best BLASTX or BLASTN hit was interpreted as gene ontology (GO) in Swiss-Prot Protein Knowledgebase (http://www.expasy.org). For a given informative feature, all of the GO terms from molecular function category (if available) were selected for gene functional annotation. If GO terms from the molecular function category were not available, all of the GO terms from the cellular component [c] category were used for gene functional annotation. Lastly, if molecular function or cellular component GO terms were not available, then all of the GO terms from the biological process [b] category were used for functional annotation. They were manually assigned to six categories in the table.

[4]Microarray mean fold change (averaging from four technical replicate arrays including two dye-swaps) and standard error of the mean (SEM) values were calculated based on normalized data from GeneSpring GX 7.3 software (Agilent Technologies). Since only technical replicates with pooled RNA samples were involved in the microarray study, microarray data SEM values convey information on technical variability (not biological variability). However the QPCR experiment incorporated biological replicates into its design; therefore, QPCR data SEM values convey information on biological variability.

[5]Wherever applicable, QPCR overall mean fold changes were calculated based on individual RQ values (Appendix VI, see Section 3.3 for details); statistically significant ($p < 0.05$) fold changes are indicated by asterisks.

functional annotation showing involvement in carbohydrate metabolism, five features were involved in lipid metabolism, seven features were involved in protein metabolism, seven features were involved in iron homeostasis, seven features were involved in immune- or stress-related responses, and the remaining nine features were involved in other biological processes (Table 2). Informative features with higher expression level in AS25 over AS11 (27 features; Appendix III) and in AS25 over AS26 (102 features; Appendix V) were compared using Venn diagrams. Only one microarray feature (representing a transcript encoding an ADAMTS-1-like protein) was identified as reproducibly more highly expressed in the slow-growing family compared with the fast-growing families in both microarray comparisons (Fig. 4C; Table 2).

To investigate the biological processes that may be associated with fast-growing families versus slow-growing family microarray gene lists, the proportion of GO terms associated with each pooled gene list (all of the genes differentially expressed in AS11 vs. AS25 or AS26 vs. AS25) in this study was compared to the overall proportion of GO terms associated with all cDNAs in the 32K microarray using Fisher's exact test. As a result, 9 and 26 biological process terms were found to be significantly ($p < 0.05$; ≥ 3 times) enriched in the list of differentially expressed transcripts that were identified in AS11 vs. AS25 and AS26 vs. AS25 comparisons, respectively (Table 3). Of these biological processes, six GO terms were significantly enriched in both comparisons (Table 3). All 35 enriched GO terms (including the six overlapping GO terms duplicated in Table 3 since they were enriched in both comparisons) were categorized into seven groups (biological regulation, cellular component organization or biogenesis, cellular process, developmental process, localization, metabolic process, and response to

Table 3. Gene ontology (GO) terms over-represented in differentially expressed transcripts between two fast-growing 3NGHTg Atlantic salmon families (AS11 and AS26) and a slow-growing 3NGHTg family (AS25).

GO ID [1]	GO Term [2]	% Test[3]	% Ref[4]	*p*-Value[5]	Comparison[6]
Biological regulation					
GO:0006879	Cellular iron ion homeostasis	6.94	0.48	<0.01	1
GO:0006879	Cellular iron ion homeostasis	4.00	0.48	<0.01	2
GO:0045069	Regulation of viral genome replication	1.09	0.13	<0.01	2
GO:0050821	Protein stabilization	4.17	0.36	<0.01	1
Cellular component organization or biogenesis					
GO:0000028	Ribosomal small subunit assembly	1.09	0.12	<0.01	2
GO:0042273	Ribosomal large subunit biogenesis	1.09	0.23	0.03	2
GO:0042989	Sequestering of actin monomers	1.09	0.10	<0.01	2
Cellular process					
GO:0051402	Neuron apoptosis	4.17	0.63	0.01	1
Developmental process					
GO:0031018	Endocrine pancreas development	7.64	2.25	<0.01	2
GO:0031100	Organ regeneration	1.09	0.26	0.03	2
GO:0045445	Myoblast differentiation	1.09	0.16	0.01	2
Localization					
GO:0002576	Platelet degranulation	1.45	0.36	0.02	2
GO:0006826	Iron ion transport	4.36	0.46	<0.01	2
GO:0006826	Iron ion transport	6.94	0.46	<0.01	1
GO:0015671	Oxygen transport	15.28	0.46	<0.01	1
GO:0015671	Oxygen transport	2.18	0.46	<0.01	2
GO:0033344	Cholesterol efflux	1.09	0.17	0.01	2
Metabolic process					
GO:0006094	Gluconeogenesis	1.45	0.31	0.01	2
GO:0006096	Glycolysis	4.00	0.73	<0.01	2

GO:0006096	Glycolysis	8.33	0.73	<0.01	1
GO:0006108	Malate metabolic process	1.09	0.12	<0.01	2
GO:0006364	rRNA processing	3.64	1.08	<0.01	2
GO:0006414	Translational elongation	11.27	3.28	<0.01	2
GO:0006415	Translational termination	7.64	2.16	<0.01	2
GO:0006559	L-phenylalanine catabolic process	1.09	0.09	<0.01	2
GO:0008203	Cholesterol metabolic process	2.18	0.56	<0.01	2
GO:0015986	ATP synthesis coupled proton transport	2.18	0.77	0.02	2
GO:0018119	Peptidyl-cysteine S-nitrosylation	4.17	0.14	<0.01	1
GO:0018119	Peptidyl-cysteine S-nitrosylation	1.09	0.14	0.01	2
GO:0019047	Provirus integration	1.09	0.10	<0.01	2
GO:0019083	Viral transcription	8.00	2.49	<0.01	2
GO:0042157	Lipoprotein metabolic process	2.55	0.74	<0.01	2
GO:0042157	Lipoprotein metabolic process	4.17	0.74	0.02	1
GO:0055114	Oxidation reduction	19.44	7.24	<0.01	1
Response to stimulus					
GO:0042742	Defense response to bacterium	1.82	0.43	0.01	2

[1]GO-ID and [2]GO identifiers of biological process terms that were associated three or more times with transcripts present in the pooled list of genes that were differentially expressed in the microarray comparison (i.e. AS11 vs. AS25 or AS26 vs. AS25). All GO terms enriched in pooled gene lists were categorized into seven groups based on biological processes at ancestral level (broadest category) in Swiss-Prot Protein Knowledgebase.

[3]Percentage of transcripts in the pooled gene list (i.e. all of the genes that were differentially expressed between families in one comparison) that are associated with the GO term.

[4]Percentage of transcripts in the 32K cGRASP cDNA microarray (i.e. 11520 annotated microarray features) that are associated with the GO term.

[5]Statistical enrichment for GO term.

[6]Pooled gene lists for which GO terms were significantly (i.e. associated three or more times with differentially expressed transcripts that were identified in one microarray comparison; $p < 0.05$) enriched. "1" represents pooled list of genes that were differentially expressed in microarray comparison AS11 vs. AS25, and "2" represents pooled list of genes that were differentially expressed in microarray comparison AS26 vs. AS25.

stimulus) based on their high-level parent terms in Swiss-Prot Protein Knowledgebase. Fourteen different biological processes related to metabolic process were among the GO terms that were significantly over-represented in fast-growing vs. slow-growing 3NGHTg microarray gene lists (Table 3).

3.4 QPCR validations of microarray results

A total of 15 microarray-identified, candidate growth-relevant TOIs were selected for QPCR studies involving individual fish templates to validate the microarray results and assess the biological variability in their mRNA expression.

3.4.1 QPCR primer design and quality control

The QPCR primers for the 15 TOIs were designed based on the alignment of informative microarray feature ESTs and available homologous nucleotide sequences in GenBank (Table 4). Specifically, QPCR primers for apolipoprotein A-IV (APOAIV), delta5-desaturase-like protein (D5DP), and nuclear protein 1 (NUPR1) were designed using Atlantic salmon sequences that are putatively orthologues to microarray features represented by rainbow trout ESTs; QPCR primers for acyl-CoA-binding protein (ACBP) and annexin 5 (AA5) were designed using Atlantic salmon sequences; QPCR primers for ferritin middle subunit (FTM) were designed using a consensus sequence since several FTM microarray features representing at least three putative paralogous FTM nucleotide sequences were identified (see Table 4 footnote for details); QPCR primers for a

Table 4. Primers for 15 QPCR transcripts of interest identified in microarray studies as being differentially expressed between fast-growing 3NGHTg Atlantic salmon families (AS11 and AS26) and a slow-growing 3NGHTg salmon family (AS25) in microarray studies and 1 normalizer gene.

Gene name[1]	QPCR					EST accession number of informative microarray features[4]	Microarray gene lists (Appendices II-V)
	Primer sequence (F: forward; R: reverse)	Sequence used for primer design[2]	Amplification efficiency (%)	Amplicon size (bp)[3]	Fig. and panel		
AA5	**F** 5' CAGTGTGAGAGCCAGTGGAA 3'	BT060178[5]	88	132	11.G	CB509241	AS11<AS25
	R 5' TGTCTCTGGCTGTTGCTACG 3'						
ADAMTS1	**F** 5' TCGGGGCAAAGTAGCTGTAT 3'	Consensus sequence[6]	99	193	11.F	CK990279	AS11<AS25 &
	R 5' AACGGCGACTACAAGCTGAT 3'						AS26<AS25
ACBP	**F** 5' GAGGTATGTGCAGGGTGGTT 3'	BT125212	90	161	11.A	CB493696	AS11>AS25 &
	R 5' CGGCTTGTTGGTCCTGTATT 3'						AS26>AS25
APOAI-1	**F** 5' AGGTGAAGTTGACTGCACAGAG 3'	BT049771	100	117	12.A	*CB494614*	AS26>AS25
	R 5' AGGTGGAATCAGCAAACTGC 3'						
APOAI-2	**F** 5' ACATGGCTCAGGTGAAGGAG 3'	BT048392	100	173	12.B	CB506105	AS26>AS25
	R 5' AGTCAACTGAGCGCCGAAG 3'					CA041892	AS11>AS25 &
							AS26>AS25
APOAIV	**F** 5' CGCTCTGGCTGTATTCACTG 3'	BT047267	89	110	11.B	*CB493958*	AS11>AS25 &
	R 5' TTGCCTTGGCAACGTAGT 3'						AS26>AS25
B2M1	**F** 5' TCCGTGCCAGCCTTAAACTA 3'	BT046451	91	186	14.A	CB500803	AS26>AS25
	R 5' TCAGAAGCTGTGCCATTTGT 3'					CB500982	AS26>AS25
						CB505594	AS11>AS25 &
							AS26>AS25
B2M2	**F** 5' GTGGCCAGCCCTACACTAGA 3'	AF180483	102	168	14.B	CK990806	AS11>AS25

	R 5' GAGGTTCCCCACACAACTTT 3'					CA061048	AS11>AS25
						CB505897	AS11>AS25
						CA043324	AS11>AS25 &
							AS26>AS25
D5DP	**F** 5' AAGGGTGACGGGCTTGAG 3'	AF478472	98	174	11.C	*CB493595*	AS11>AS25 &
	R 5' GTGACTGATGACCCTGATGC 3'						AS26>AS25
FTM	**F** 5' TCAAGGAGAACAGCGACGAG 3'	Consensus sequence[7]	95	100	11.D	CB510731	AS11>AS25 &
	R 5' GGCTTCTTGATGTCCTGGAG 3'						AS26>AS25
						CB506201	AS11>AS25
						CB502663	AS26>AS25
						CA042437	AS26>AS25
						CB505282	AS26>AS25
GAPDH1	**F** 5' GAGGTCGTCGCCATCAAT 3'	BT046468	102	141	13.A	CB510408	AS11>AS25
	R 5' GATGTGCAGATTGCCAATGA 3'						
GAPDH2	**F** 5' CGCCAAGAGTGGAAAAGTTG 3'	BT050045	104	163	13.B	CB514460	AS11>AS25
	R 5' TGTGATGTGGAGGTTTCCAA 3'					BU965756	AS11>AS25 &
							AS26>AS25
NUPR1	**F** 5' GAGAAACACCCGTGGAAAAA 3'	BT048359	92	147	11.E	*CB490586*	AS11>AS25 &
	R 5' GTGGGTTGGCTCAACATTCT 3'						AS26>AS25
SEPP1	**F** 5' TCCGGTACTGTAAAGCCACA 3'	BT072678	100	158	15.A	CA040124	AS11>AS25
	R 5' GTGGAGGCTACCTTCCTTGA 3'					CB505935	AS11>AS25
						CA769454	AS26>AS25
SEPP2	**F** 5' AGACCCTGGCTGGAGAGAAG 3'	BT072221	98	156	15.B	CA049981	AS26>AS25
	R 5' ACGAGCAGTCACCACAGATG 3'					CB498862	AS26>AS25
PABP1	**F** 5' TGACCGTCTCGGGTTTTTAG 3'	CA052954[8]	102	108		CA052954	
(Normalizer)	**R** 5' CCAAGGTGGATGAAGCTGTT 3'						

[1]Transcripts selected from microarray gene lists (Appendices II-V) that were differentially expressed between fast-growing 3NGHTg Atlantic salmon families (AS11 and AS25) and a slow-growing 3NGHTg salmon family (AS25). Two transcripts of interests (AA5 and ADAMTS1) were associated with slow-growing families and the remaining thirteen transcripts of interest were highly expressed in at least one fast-growing family compared with the slow-growing family.

[2]The accession numbers for Atlantic salmon NCBI nucleotide database entries that were used to design QPCR primers are listed. For APOAI, B2M, GAPDH, and SEPP, paralogue-specific primers were designed based on nucleotide sequence alignments at the nucleotide level (see Fig. 5-8 for sequence alignment results and primer locations).

[3]QPCR products amplified with each primer pair were electrophoretically separated on an ethidium bromide-stained agarose gel (2%) alongside a 100 bp ladder (Invitrogen) to confirm that amplified products were of the expected size (Fig. 10).

[4]Microarray features (Atlantic salmon ESTs) more than 95% identical to the nucleotide sequences that were used to design QPCR primers are listed in regular font. Microarray features represented by rainbow trout ESTs are in italics; their putative Atlantic salmon orthologues (best BLASTn hit from Atlantic salmon) were used for the design of QPCR primers.

[5]Although nucleotide BT060178 is the closest nucleotide sequence to the microarray feature CB509241, multiple alignment analysis suggests that CB509241 represents a putative splice variant of BT060178.

[6]Five sets of primer pairs were designed for ADAMTS1 (CK990279), but none of them passed quality testing for QPCR study (e.g. due to low amplification efficiency or multiple peaks in melt curve). Nucleotide sequence representing Atlantic salmon ADAMTS-1 is not available in the NCBI nucleotide database. Therefore, its QPCR primers were designed based on a consensus sequence (greater than 96.8% identity between any two contributing sequences) among homologous ESTs (i.e. BLASTn against NCBI EST database) with the following GenBank ID: CK990279, DW546792, DW549716, DW563041, DY696604, DY711996.

[7]Several FTM-like microarray features possibly representing at least 3 putative paralogous FTM nucleotide sequences were identified. In order to avoid biased QPCR result towards a certain set of paralogues, generic QPCR primers were designed (GenBank ID: BT045310, BT046912, BT049618, CB502663) to amplify these putative FTM paralogues.

[8]QPCR primer of PABP1 was designed from microarray feature CA052954 as this feature was stably ($0.9 < \text{fold-change} < 1.4$) expressed in seven out of eight arrays in microarray study.

disintegrin and metalloprotease with thrombospondin motifs-1 (ADAMTS1) were designed using consensus sequences since the primers designed from the informative microarray feature did not pass quality testing for QPCR study (see Table 4 footnotes for details). Additionally, paralogue-specific primers were designed for four microarray-identified genes (apolipoprotein A-I (APOAI), beta2-microglobulin (B2M), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and selenoprotein Pa (SEPP)) since microarray features encoding these potentially growth-relevant genes were reproducibly associated with fast-growing families and were represented by divergent sequences that suggested the possibility of paralogues. The QPCR primers for the four putative paralogous pairs were designed from Atlantic salmon sequences that were greater than 95% identical to Atlantic salmon microarray features (APOAI-2, B2M, GAPDH, and SEPP) or rainbow trout microarray features (APOAI-1) (Table 4). Nucleotide sequences used for paralogue-specific QPCR primer design were aligned in MegAlign software using the Clustal W program, giving the following results: APOAI-1 (GenBank ID: BT049771) was 89% identical to APOAI-2 (GenBank ID: BT048392) with 15% nucleotide differences in both forward primers and APOAI-2 reverse primer, and 25% nucleotide differences in APOAI-1 reverse primer (Fig. 5; Table 5); B2M1 (GenBank ID: BT046451) was 68% identical to B2M2 (GenBank ID: AF180483) with at least 65% nucleotide differences in both forward and reverse primers (Fig. 6; Table 5); GAPDH1 (GenBank ID: BT046468) was 91% identical to GAPDH2 (GenBank ID: BT050045) with 10% and 25% nucleotide differences in GAPDH1 and GAPDH2 forward primers, respectively, and 15% nucleotide differences in both reverse primers

Table 5. Percent identities of four sets of paralogues at nucleotide and hypothetical amino acid levels.

Gene Name	Sequence used for primer design	Percent identity (%)	
		Nucleotide level[1]	Hypothetical amino acid level[2]
APOAI-1	BT049771	89	83
APOAI-2	BT048392		
B2M1	BT046451	68	91
B2M2	AF180483		
GAPDH1	BT046468	91	99
GAPDH2	BT050045		
SEPP1	BT072678	83	N/A[3]
SEPP2	BT072221		

[1]Percent identity of each paralogue set at the nucleotide level was determined by Clustal W method in MegAlign software (DNASTAR). See sequence alignments in Figures 5-8.
[2]Percent identity of each paralogue set at the hypothetical amino acid level was determined by BLASTp two sequences (NCBI).
[3]The protein entry for *Salmo salar* SEPP is not available in NCBI protein database (see Section 3.1 for details).

Fig. 5. Sequence alignment of Atlantic salmon nucleotide sequences of putative paralogues apolipoprotein A-I type 1 (APOAI-1) and apolipoprotein A-I type 2 (APOAI-2). This alignment report was generated from MegAlign software (DNASTAR) using the Clustal W program. The paralogue-specific QPCR primers are shaded in grey. Nucleotide differences between sequences in the primer-design region are indicated by arrows.

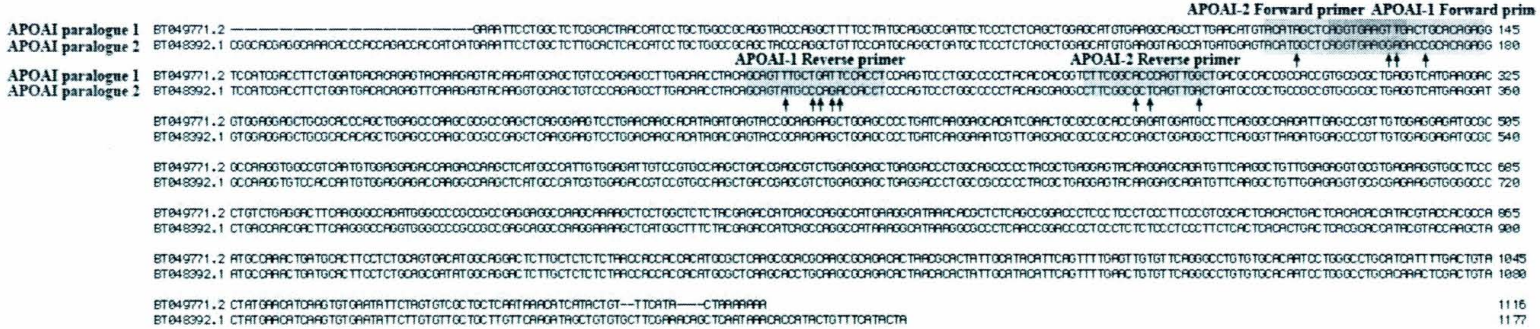
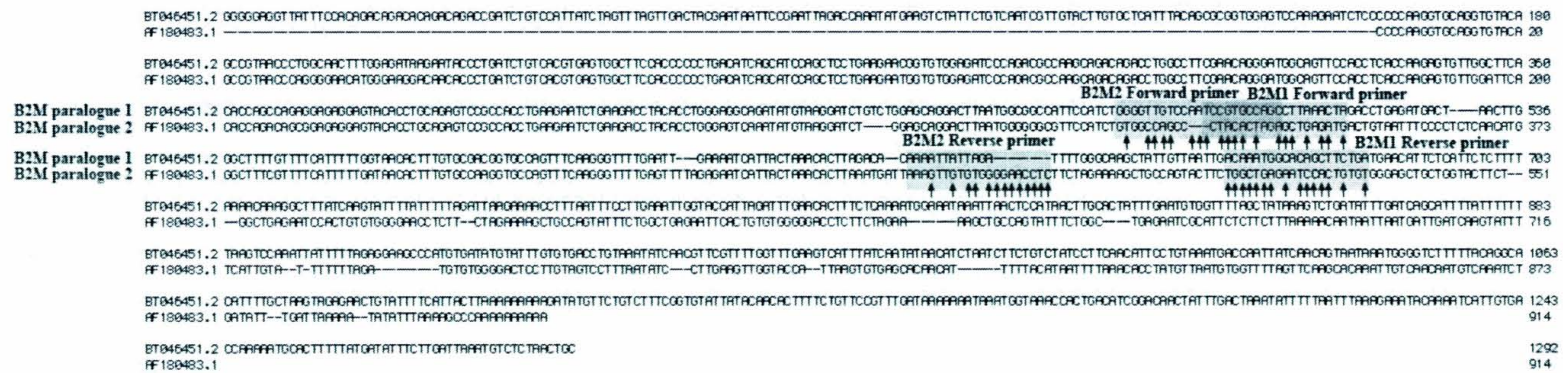

APOAI-2 Forward primer
APOAI-1 Forward prim
APOAI paralogue 1
APOAI paralogue 2
APOAI-1 Reverse primer
APOAI-2 Reverse primer

Fig. 6. Sequence alignment of Atlantic salmon nucleotide sequences of putative paralogues beta-2 microglobulin type 1 (B2M1) and beta-2 microglobulin type 2 (B2M2). This alignment report was generated from MegAlign software (DNASTAR) using the Clustal W program. The paralogue-specific QPCR primers are shaded in grey. Nucleotide differences between sequences in the primer-design region are indicated by arrows.


B2M2 Forward primer
B2M1 Forward primer
B2M paralogue 1
B2M paralogue 2
B2M2 Reverse primer
B2M1 Reverse primer

(Fig. 7; Table 5); SEPP1 (GenBank ID: BT072678) was 83% identical to SEPP2 (GenBank ID: BT072221) with 30% and 20% nucleotide differences in SEPP1 forward and reverse primers, respectively, and 10% nucleotide differences in both SEPP2 forward and reverse primers (Fig. 8; Table 5).

The similarities of the four paralogue pairs at the hypothetical amino acid level were also determined in the current study. Nucleotide sequences were firstly translated to hypothetical amino acid sequences using translate tool of Swiss-Prot., and the correct hypothetical amino acid sequences was then selected by searching the translations against non-redundant (nr) protein database using BLASTp. The similarities of paralogues at the amino acid level were determined by aligning two hypothetical amino acid sequences that were translated from TOIs using BLASTp (Table 5). As a result, APOAI-1 was 83% identical to APOAI-2 at the hypothetical amino acid level over 242 aligned amino acid residues (E-value: 2e-148); B2M1 was 91% identical to B2M2 at the hypothetical amino acid level over 93 aligned amino acid residues (E-value: 4e-66); GAPDH1 was 99% identical to GAPDH2 at the hypothetical amino acid level over 334 aligned amino acid residues (E-value: 0). The data mining of SEPP paralogue pair suggested they were putative pseudogenes. Their best BLASTx hits were zebrafish selenoprotein P protein (accession number: AAI55822). SEPP1 was 58% identical to this best hit at the hypothetical amino acid level over 169 aligned amino acid residues (E-value: 1e-54), and SEPP2 was 62% identical to this best hit at the hypothetical amino acid level over 174 aligned amino acid residues (E-value: 2e-58).

Fig. 7. Sequence alignment of Atlantic salmon nucleotide sequences of putative paralogues glyceraldehyde-3-phosphate dehydrogenase type 1 (GAPDH1) and glyceraldehyde-3-phosphate dehydrogenase type 2 (GAPDH2). This alignment report was generated from MegAlign software (DNASTAR) using the Clustal W program. The paralogue-specific QPCR primers are shaded in grey. Nucleotide differences between sequences in the primer-design region are indicated by arrows.

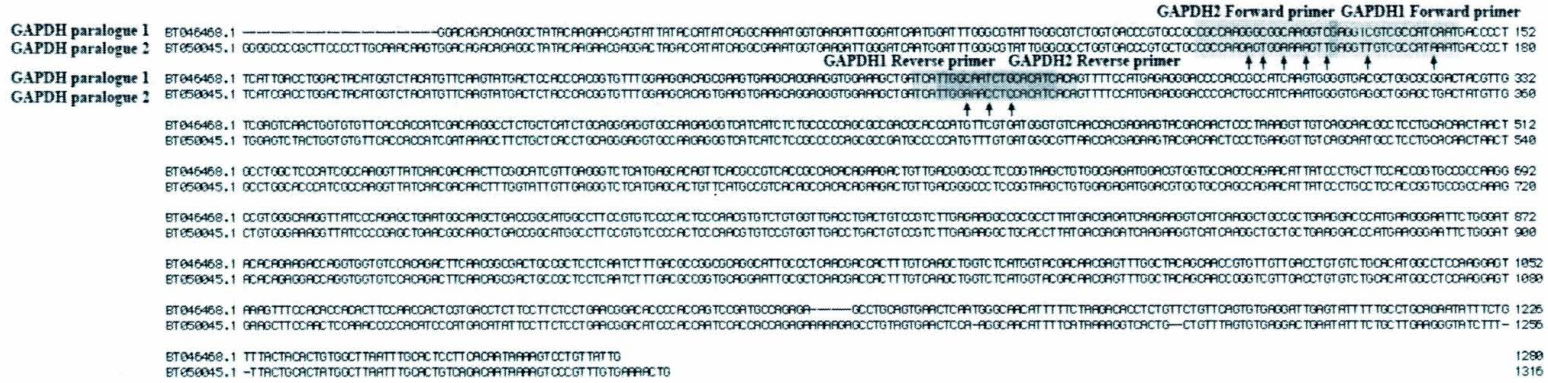
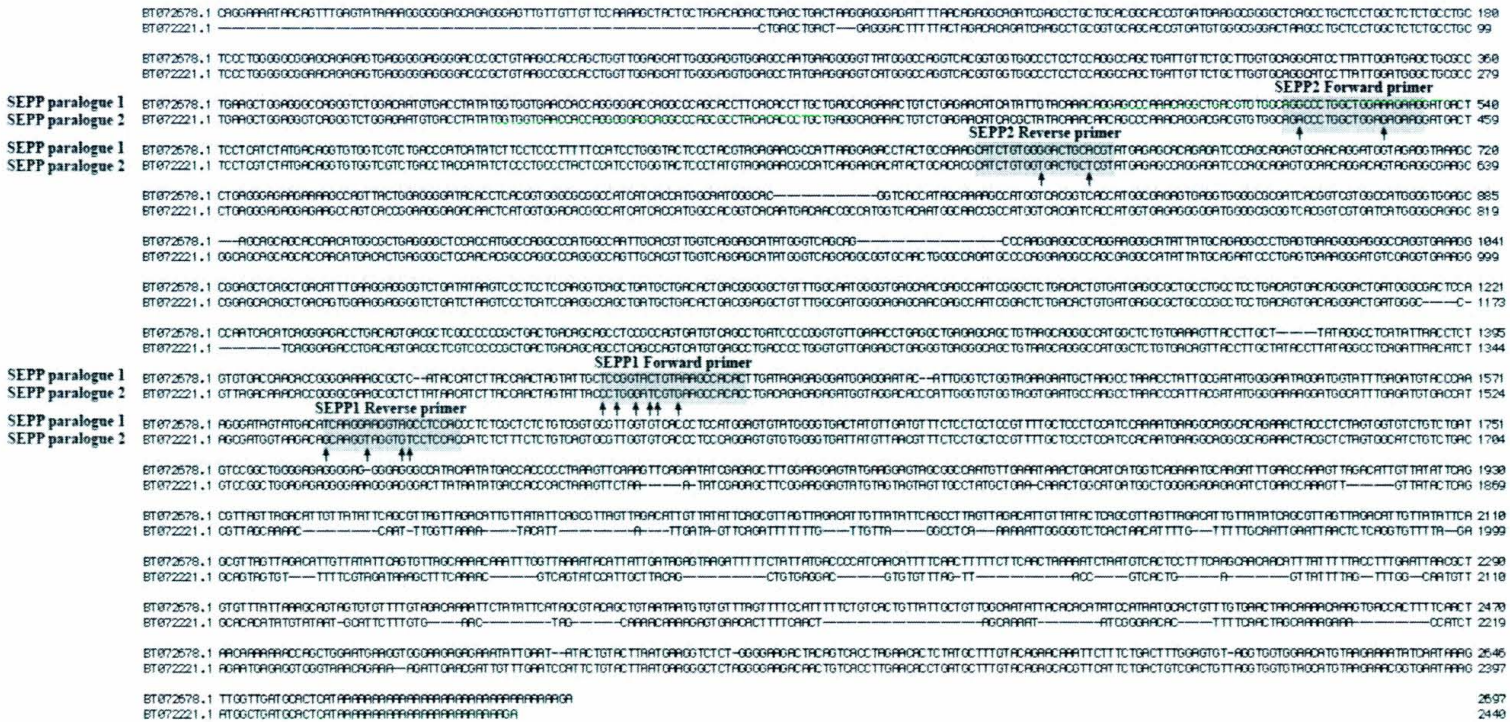

GAPDH2 Forward primer
GAPDH1 Forward primer
GAPDH paralogue 1
GAPDH paralogue 2
GAPDH1 Reverse primer
GAPDH2 Reverse primer

Fig. 8. Sequence alignment of Atlantic salmon nucleotide sequences of putative paralogues selenoprotein Pa type 1 (SEPP1) and selenoprotein Pa type 2 (SEPP2). This alignment report was generated from MegAlign software (DNASTAR) using the Clustal W program. The paralogue-specific QPCR primers are shaded in grey. Nucleotide differences between sequences in the primer-design region are indicated by arrows.


SEPP2 Forward primer
SEPP2 Reverse primer
SEPP1 Forward primer
SEPP1 Reverse primer
SEPP paralogue 1
SEPP paralogue 2
SEPP paralogue 1
SEPP paralogue 2
SEPP paralogue 1
SEPP paralogue 2

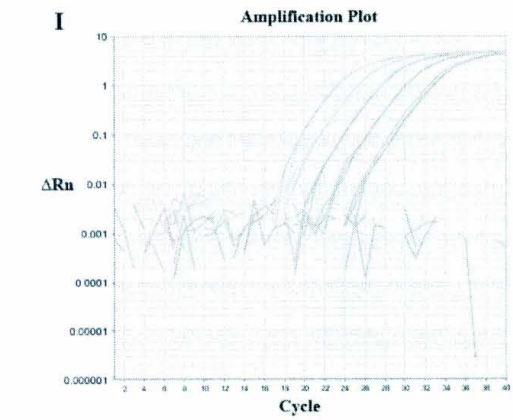
Quality control (QC) testing was conducted for each QPCR primer pair. The results of primer QC for the D5DP primer pair are shown as an example (Fig. 9A). D5DP QPCR primer QC results indicated 98.31% amplification efficiency ($r^2 = 0.998$) (Fig. 9A. II; see Section 2.7 for details). A single sharp peak at the expected melting temperature observed in the D5DP amplicon melt curve indicated high specificity of the amplification and the absence of primer dimers (Fig. 9A. III). Similarly, the melt curve of the normalizer PABP1 primer pair had a single sharp peak at the expected melting temperature and the amplification efficiency for this primer was 101.78% ($r^2 = 0.999$) (Fig. 9B). The QPCR primer QC testing results for all TOIs and the normalizer gene are listed in Table 4. Furthermore, the QPCR amplicon size for each primer pair was demonstrated by 2% agarose gel electrophoresis to show sharp, single bands at the expected size (Fig. 10; Table 4).

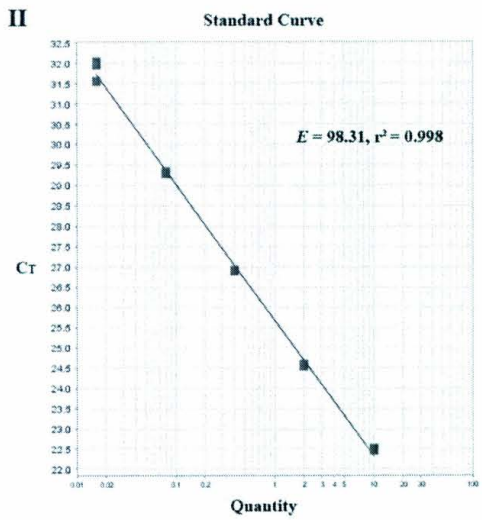
3.4.2 Comparison of QPCR and microarray results

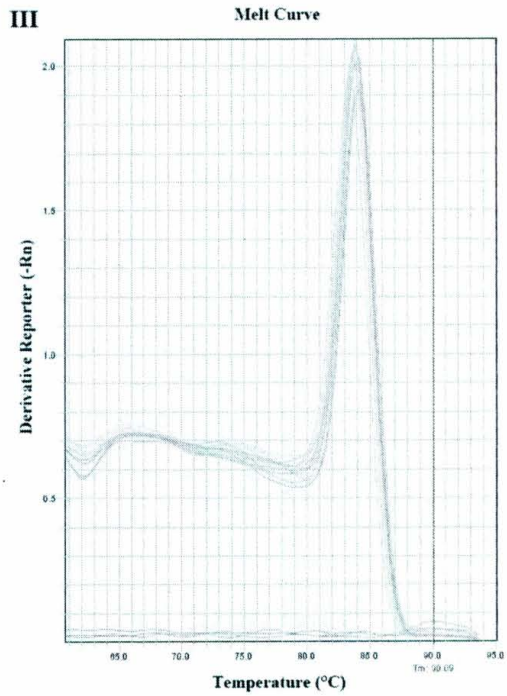
Of the 15 transcripts subjected to QPCR, 13 were determined to be associated with fast-growing 3NGHTg salmon families in the microarray study (Appendices II and IV). These were: ACBP, APOAI-1, APOAI-2, APOAIV, B2M1, B2M2, D5DP, FTM, GAPDH1, GAPDH2, NUPR1, SEPP1, and SEPP2. The remaining two transcripts, AA5 and ADAMTS1, were determined to be associated with slow-growing 3NGHTg salmon family in the microarray study (Appendices III and V).

Fig. 9. Examples of QPCR primer quality control (A. Delta5-desaturase-like protein, D5DP; B. Polyadenylate-binding protein, PABP1). I. Amplification plots for five 1:5 serial dilutions of pooled cDNA (starting with cDNA corresponding to 10 ng of input total RNA) with equal contributions by all individuals involved in the QPCR study. II. Standard curves for the five 1:5 serial dilutions of pooled cDNA, indicating efficiency of amplification. For D5DP, efficiency E = 98.31%, r^2 = 0.998. For PABP1, efficiency E = 101.78%, r^2 = 0.999. III. Melt curves for detecting primer-dimers or non-specific amplification. The single peak of melt curve at the expected melting temperature of the amplicon indicates high specificity of this amplification.

A.

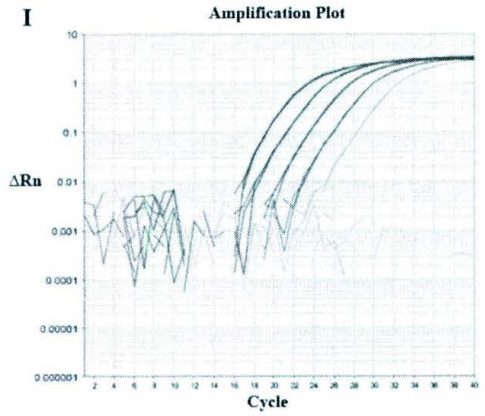

I
Amplification Plot
ΔRn
Cycle


II
Standard Curve
E = 98.31, r² = 0.998
CT
Quantity

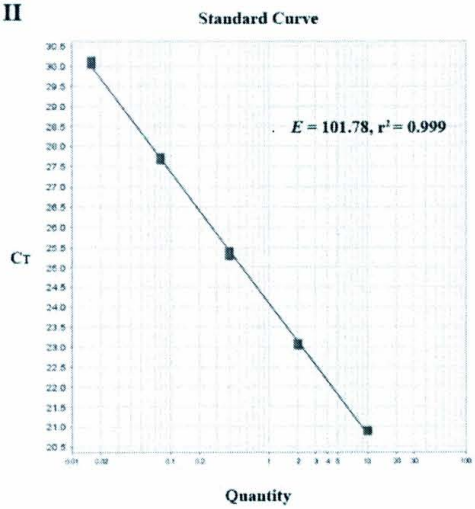

III
Melt Curve
Derivative Reporter (-Rn)
Temperature (°C)

B.

I


Amplification Plot
ΔRn
Cycle

II


Standard Curve
E = 101.78, r² = 0.999
CT
Quantity

III

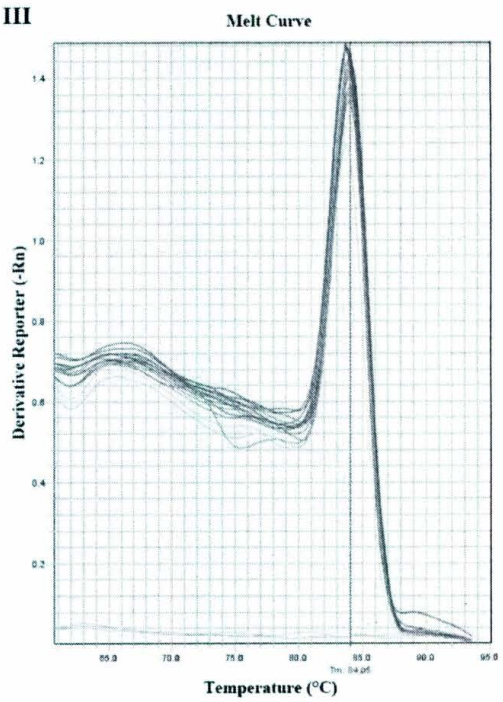
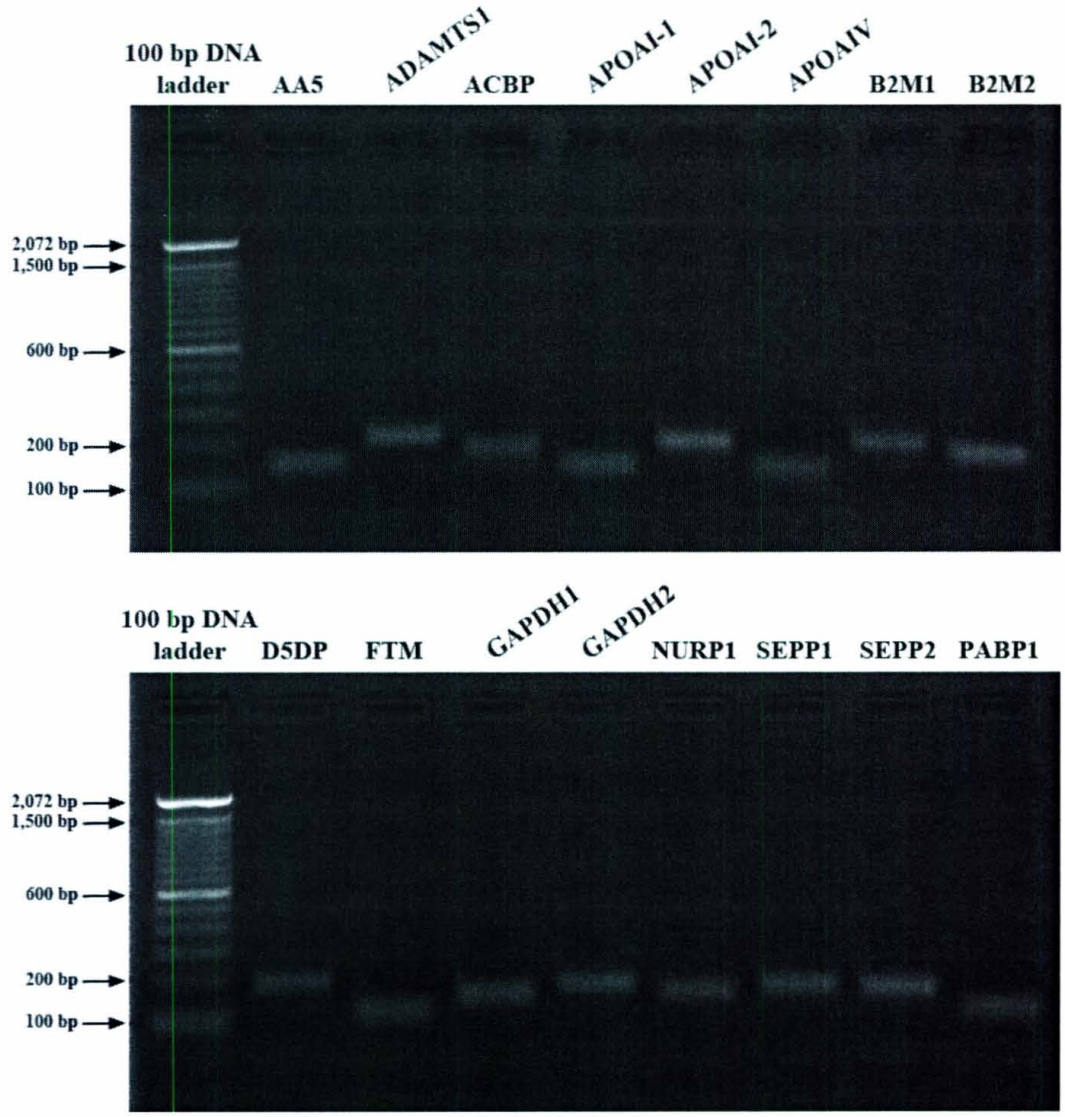

Melt Curve
Derivative Reporter (-Rn)
Temperature (°C)

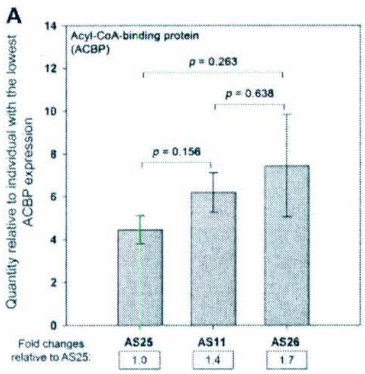
Fig. 10. Image of an ethidium bromide-stained agarose gel showing electrophoretically separated QPCR amplicons generated from QPCR assay of a liver cDNA sample (fish number 155) from 3NGHTg Atlantic salmon family AS11. The resulting QPCR products were electrophoretically separated on a 2% agarose gel stained with ethidium bromide to confirm the correct sizes of amplified products (see Table 4 for amplicon sizes). Size marker (100 bp DNA ladder; Invitrogen) and abbreviations of gene names that associated with primer pairs are indicated above each gel lane.

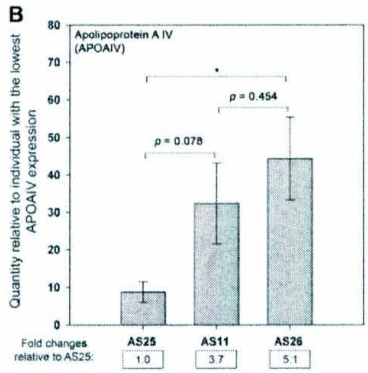

100 bp DNA ladder
AA5
ADAMTS1
ACBP
APOAI-1
APOAI-2
APOAIV
B2M1
B2M2
2,072 bp
1,500 bp
600 bp
200 bp
100 bp
100 bp DNA ladder
D5DP
FTM
GAPDH1
GAPDH2
NURP1
SEPP1
SEPP2
PABP1
2,072 bp
1,500 bp
600 bp
200 bp
100 bp

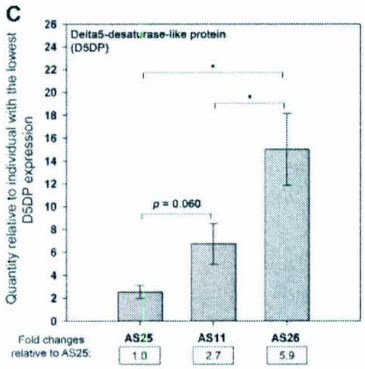
Many of the transcripts selected for these QPCR studies have functional annotations suggesting involvement in metabolism, iron homeostasis, cellular process, and immune- or stress-related biological processes (Table 2). For each TOI, the QPCR study was conducted using templates reverse transcribed from individual liver total RNA samples (biological replicate) from all three 3NGHTg Atlantic salmon families (AS11, AS26, and AS25). Expression levels of a given transcript in the different studied families were shown as mean relative quantities (RQs) ± SEM (see Section 2.7 for details on calculation; see Appendix VI for individual RQ values). The overall fold change values in Table 2 and Figures 11-15 refer to ratios between average RQs from a fast-growing family (AS11 or AS26) and the slow-growing family (AS25).

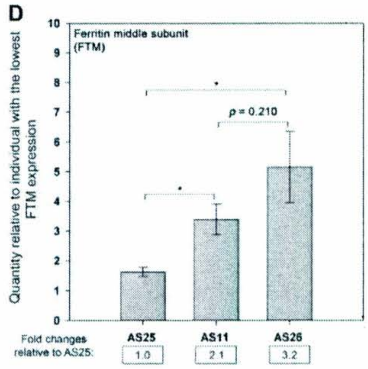
The QPCR results largely agreed with the microarray results as 12 of the 13 microarray-identified, putative enhanced growth-related transcripts had higher expression (though not always significantly higher, see Figures 11-15) in both fast-growing 3NGHTg salmon families in the QPCR study (AS11 and AS26) in comparison to the slow-growing family (AS25). Although identified by the microarray study as more highly expressed in both fast-growing families, QPCR results for NUPR1 showed no difference in expression between AS11 (fast-growing) and AS25 (slow-growing), and 2.2-fold non-significantly (p = 0.074) higher expression in AS26 (fast-growing) compared with both AS11 and AS25 (Fig. 11E).

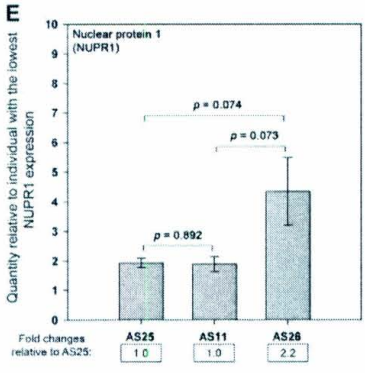
Fig. 11. QPCR results for transcripts of interest (TOIs) selected from the 32K cDNA microarray study. Mean relative quantities (RQs) with associated standard error of the mean (SEM) values are shown for three 3NGHTg Atlantic salmon families: AS25 (slow-growing), AS11 (fast-growing), and AS26 (fast-growing). Significant differences ($p < 0.05$) of expression level (RQ) between families for a single TOI are indicated by asterisks; non-significant differences ($p \geq 0.05$) are indicated as values. Overall fold change values for each TOI in families AS11 and AS26 were calculated relative to its expression level (mean RQ) in family AS25; fold change values in black font on a white background represent fold higher expression in AS11 or AS26 compared with AS25. If overall fold change values were less than 1.0, then the inverse of the fold change was calculated; fold change values in white font on a black background represent fold lower expression in AS11 or AS26 compared with AS25.

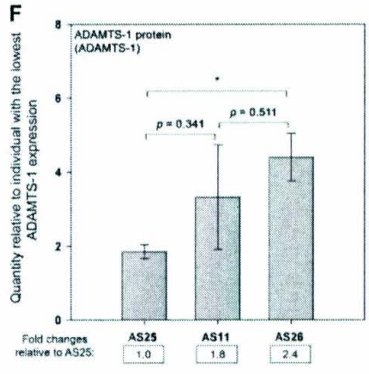

A
Acyl-CoA-binding protein
(ACBP)
p = 0.263
p = 0.638
p = 0.156
Quantity relative to individual with the lowest ACBP expression
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
1.4
1.7


B
Apolipoprotein A IV
(APOAIV)
*
p = 0.454
p = 0.078
Quantity relative to individual with the lowest APOAIV expression
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
3.7
5.1


C
Delta5-desaturase-like protein
(D5DP)
*
*
p = 0.060
Quantity relative to individual with the lowest D5DP expression
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
2.7
5.9


D
Ferritin middle subunit
(FTM)
*
p = 0.210
*
Quantity relative to individual with the lowest FTM expression
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
2.1
3.2


E
Nuclear protein 1
(NUPR1)
p = 0.074
p = 0.073
p = 0.892
Quantity relative to individual with the lowest NUPR1 expression
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
1.0
2.2


F
ADAMTS-1 protein
(ADAMTS-1)
*
p = 0.341
p = 0.511
Quantity relative to individual with the lowest ADAMTS-1 expression
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
1.8
2.4

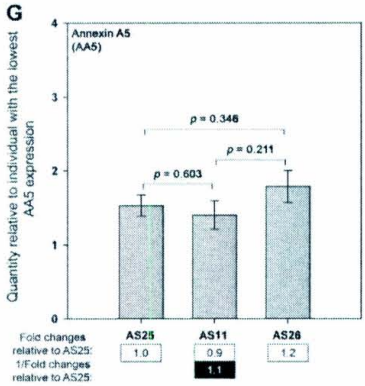
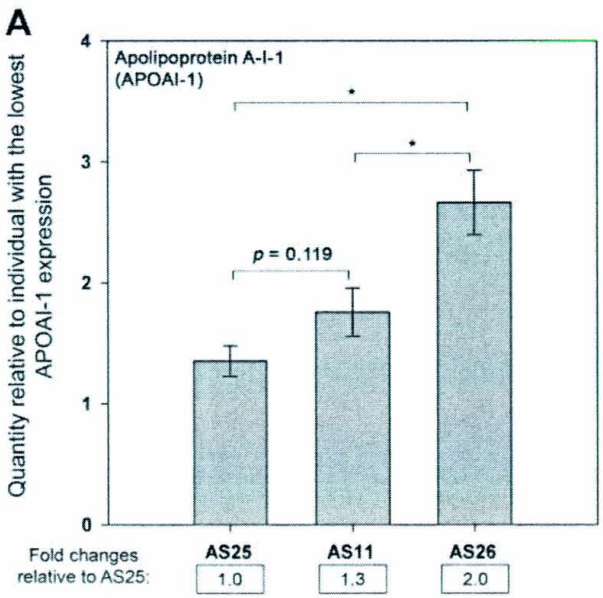

G
Annexin A5
(AA5)
p = 0.346
p = 0.211
p = 0.603
Quantity relative to individual with the lowest AA5 expression
Fold changes relative to AS25:
1/Fold changes relative to AS25:
AS25
AS11
AS26
1.0
0.9
1.1
1.2

Fig. 12. QPCR results for apolipoprotein A-I type 1 (APOAI-1) and apolipoprotein A-I type 2 (APOAI-2) selected from the 32K cDNA microarray study. Mean relative quantities (RQs) with associated standard error of the mean (SEM) values are shown for three 3NGHTg Atlantic salmon families: AS25 (slow-growing), AS11 (fast-growing), and AS26 (fast-growing). Significant differences ($p < 0.05$) of expression level (RQ) between families for APOAI-1 or APOAI-2 are indicated by asterisks; non-significant differences ($p \geq 0.05$) are indicated as values. Overall fold change values for each TOI in families AS11 and AS26 were calculated relative to expression level (mean RQ) in family AS25; fold change values in black font on a white background represent fold higher expression in AS11 or AS26 compared with AS25.


A
Apolipoprotein A-I-1
(APOAI-1)
Quantity relative to individual with the lowest APOAI-1 expression
0
1
2
3
4
*
*
p = 0.119
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
1.3
2.0

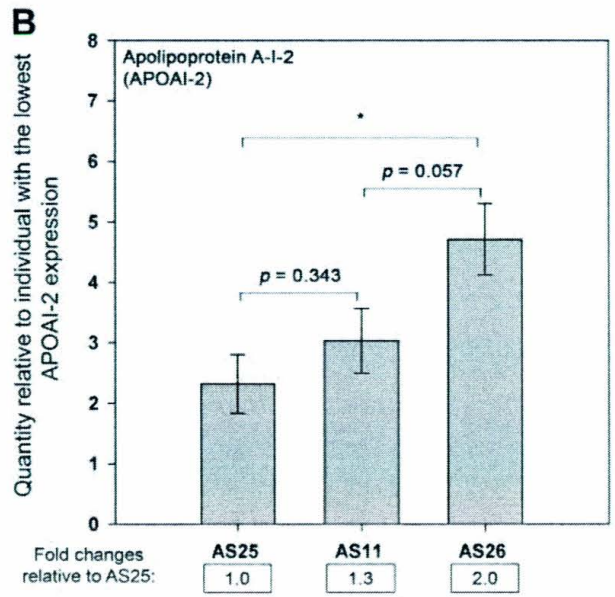
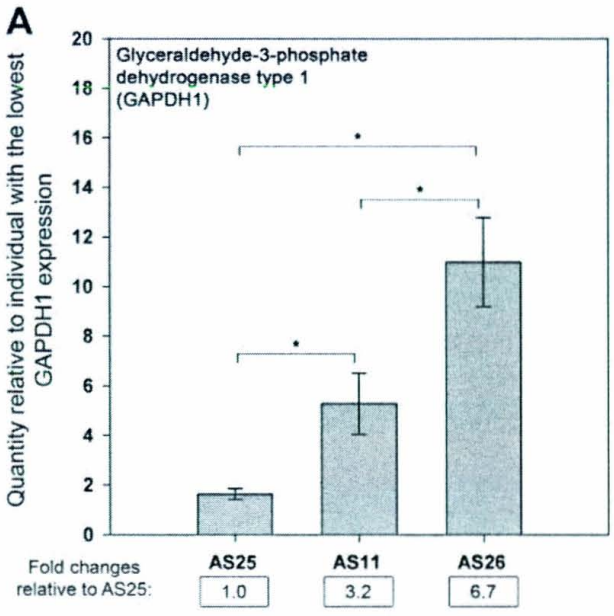

B
Apolipoprotein A-I-2
(APOAI-2)
Quantity relative to individual with the lowest APOAI-2 expression
0
1
2
3
4
5
6
7
8
*
p = 0.057
p = 0.343
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
1.3
2.0

Fig. 13. QPCR results for glyceraldehyde-3-phosphate dehydrogenase type 1 (GAPDH1) and glyceraldehyde-3-phosphate dehydrogenase type 2 (GAPDH2) selected from the 32K cDNA microarray study. Mean relative quantities (RQs) with associated standard error of the mean (SEM) values are shown for three 3NGHTg Atlantic salmon families: AS25 (slow-growing), AS11 (fast-growing), and AS26 (fast-growing). Significant differences ($p < 0.05$) of expression level (RQ) between families for GAPDH1 or GAPDH2 are indicated by asterisks; non-significant differences ($p \geq 0.05$) are indicated as values. Overall fold change values for each TOI in families AS11 and AS26 were calculated relative to its expression level (mean RQ) in family AS25; fold change values in black font on a white background represent fold higher expression in AS11 or AS26 compared with AS25.


A
Glyceraldehyde-3-phosphate dehydrogenase type 1 (GAPDH1)
Quantity relative to individual with the lowest GAPDH1 expression
0
2
4
6
8
10
12
14
16
18
20
*
*
*
Fold changes relative to AS25:
AS25
1.0
AS11
3.2
AS26
6.7

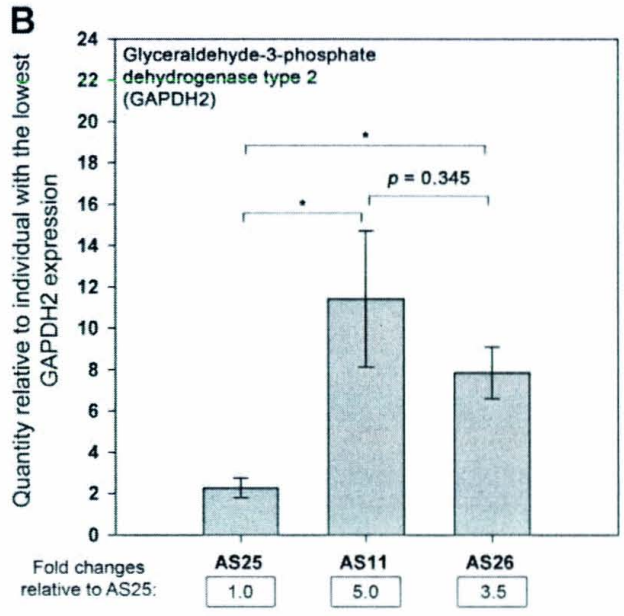
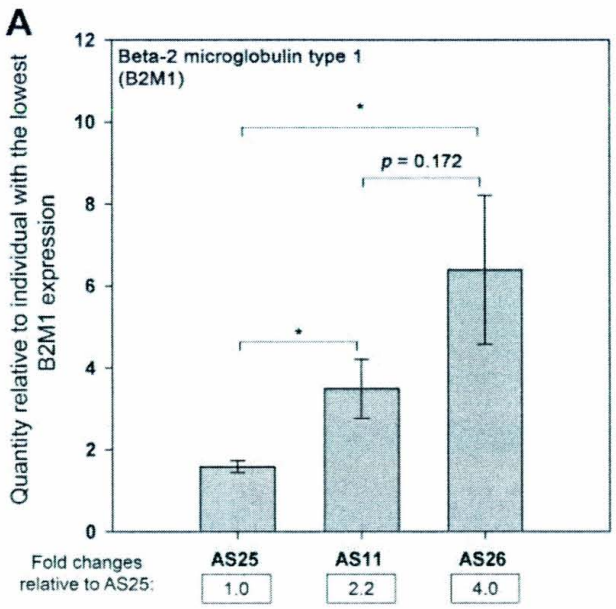

B
Glyceraldehyde-3-phosphate dehydrogenase type 2 (GAPDH2)
Quantity relative to individual with the lowest GAPDH2 expression
0
2
4
6
8
10
12
14
16
18
20
22
24
*
*
p = 0.345
Fold changes relative to AS25:
AS25
1.0
AS11
5.0
AS26
3.5

Fig. 14. QPCR results for beta-2 microglobulin type 1 (B2M1) and beta-2 microglobulin type 2 (B2M2) selected from the 32K cDNA microarray study. Mean relative quantities (RQs) with associated standard error of the mean (SEM) values are shown for three 3NGHTg Atlantic salmon families: AS25 (slow-growing), AS11 (fast-growing), and AS26 (fast-growing). Significant differences ($p < 0.05$) of expression level (RQ) between families for B2M1 or B2M2 are indicated by asterisks; non-significant differences ($p \geq 0.05$) are indicated as values. Overall fold change values for each TOI in families AS11 and AS26 were calculated relative to its expression level (mean RQ) in family AS25; fold change values in black font on a white background represent fold higher expression in AS11 or AS26 compared with AS25.


A
Beta-2 microglobulin type 1
(B2M1)
Quantity relative to individual with the lowest B2M1 expression
12
10
8
6
4
2
0
*
*
p = 0.172
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
2.2
4.0

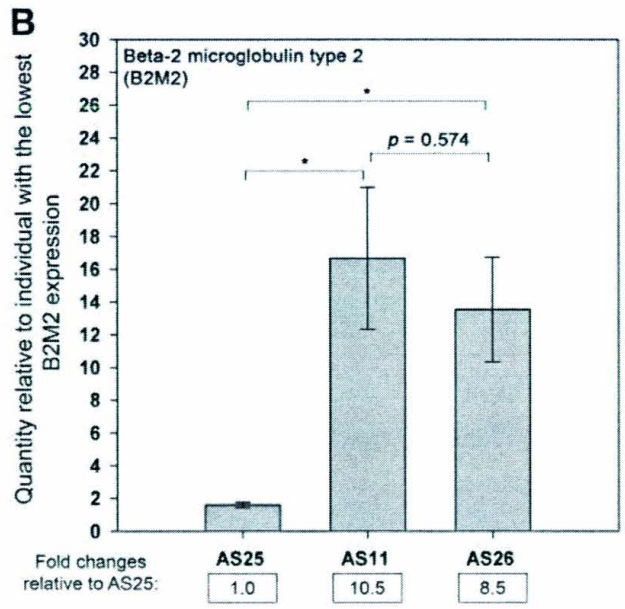
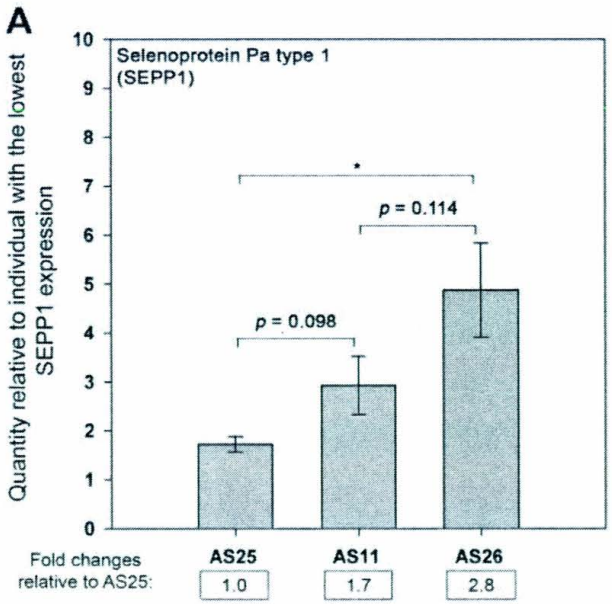
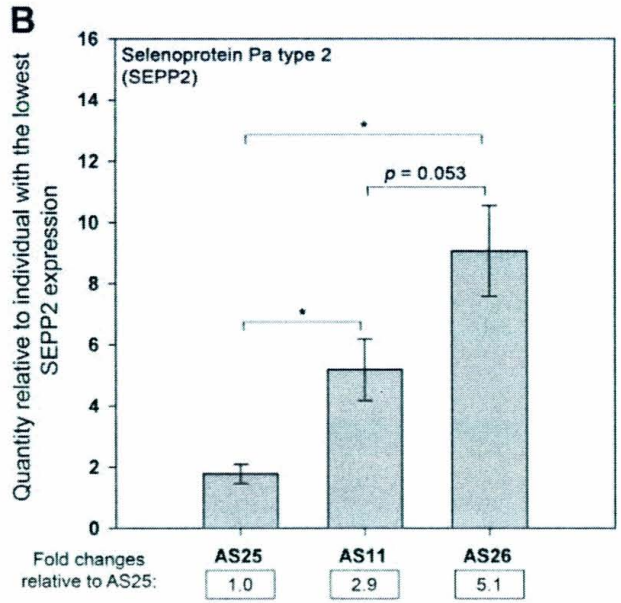

B
Beta-2 microglobulin type 2
(B2M2)
Quantity relative to individual with the lowest B2M2 expression
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
*
*
p = 0.574
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
10.5
8.5

Fig. 15. QPCR results for selenoprotein Pa type 1 (SEPP1) and selenoprotein Pa type 2 (SEPP2) selected from the 32K cDNA microarray study. Mean relative quantities (RQs) with associated standard error of the mean (SEM) values are shown for three 3NGHTg Atlantic salmon families: AS25 (slow-growing), AS11 (fast-growing), and AS26 (fast-growing). Significant differences ($p < 0.05$) of expression level (RQ) between families for SEPP1 or SEPP2 are indicated by asterisks; non-significant differences ($p \geq 0.05$) are indicated as values. Overall fold change values for each TOI in families AS11 and AS26 were calculated relative to its expression level (mean RQ) in family AS25; fold change values in black font on a white background represent fold higher expression in AS11 or AS26 compared with AS25.


A
Selenoprotein Pa type 1
(SEPP1)
Quantity relative to individual with the lowest SEPP1 expression
10
9
8
7
6
5
4
3
2
1
0
*
p = 0.114
p = 0.098
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
1.7
2.8


B
Selenoprotein Pa type 2
(SEPP2)
Quantity relative to individual with the lowest SEPP2 expression
16
14
12
10
8
6
4
2
0
*
p = 0.053
*
Fold changes relative to AS25:
AS25
AS11
AS26
1.0
2.9
5.1

Seven of the QPCR confirmed transcripts that were more highly expressed (though not always significantly higher, see Figures 11-15) in fast-growing families compared with a slow-growing family were associated with the GO term "metabolic process" (Appendices II and IV). ACBP (GO:0000062, Fatty-acyl-CoA binding) was 1.4 and 1.7 fold more highly expressed in AS11 ($p = 0.156$) and AS26 ($p = 0.263$), respectively, compared with AS25 (Fig. 11A); APOAIV (GO:0008289, Lipid binding) was 3.7 and 5.1 fold more highly expressed in AS11 ($p = 0.078$) and AS26 ($p < 0.05$), respectively, compared with AS25 (Fig. 11B); and D5DP (GO:0020037, Heme binding; GO:0016717, Oxidoreductase activity) was 2.7 and 5.9 fold more highly expressed in AS11 ($p = 0.060$) and AS26 ($p < 0.05$), respectively, compared with AS25, (Fig. 11C).

Paralogues APOAI-1 and APOAI-2 (GO:0008289, Lipid binding) were identified in the microarray studies as being more highly expressed in at least one of the two fast-growing 3NGHTg Atlantic salmon families (AS11 and AS26) compared with the slow-growing family (AS25) (Table 2; Appendices II and IV). QPCR showed that mRNA expression levels of APOAI-1 and APOAI-2 were lowest in AS25, highest in AS26 (2-fold higher than AS25), and intermediate in AS11 (1.3-fold higher than AS25) (Fig. 12). The QPCR mRNA expression of APOAI-1 in AS26 was significantly different from that in AS25 and AS11, but no significant difference ($p = 0.119$) was observed in expression between AS25 and AS11 (Fig. 12A). The QPCR mRNA expression of APOAI-2 in AS26 was significantly different from that in AS25, while expression of APOAI-2 in AS11 was no significantly different ($p = 0.343$ between AS11 and AS25; $p = 0.057$ between AS11 and AS26) from that of the other two families (Fig. 12B).

GAPDH-like transcripts (GO:0004365, phosphorylating activity) were more highly expressed in two fast-growing families when compared with the slow-growing family in the microarray studies (Table 2; Appendices II and IV). In the QPCR study, GAPDH1 mRNA expression was lowest in AS25, highest in AS26 (6.7-fold significantly higher than AS25), and intermediate in AS11 (3.2-fold significantly higher than AS25); mRNA expression of this GAPDH paralogue in each family was significantly different from that of the other families (Fig. 13A). The QPCR expression profile of GAPDH2 was different from that of GAPDH1. GAPDH2 mRNA expression was lowest in AS25, highest in AS11 (5.0-fold significantly higher than AS25), and intermediate in AS26 (3.5-fold significantly higher than AS25), and no significant difference (p = 0.345) was observed between AS11 and AS26 (Fig. 13B).

Of the transcripts with immune- or stress-related annotations, QPCR mRNA expression of B2M1 and its putative paralogue B2M2 (GO:0042612, MHC class I protein complex) confirmed the microarray results as they were both significantly more highly expressed in fast-growing families (AS11 and AS26) compared with the slow-growing family (AS25) in the QPCR study (Fig. 14; Table 2; Appendices II and IV). B2M1 mRNA expression was lowest in AS25, highest in AS26 (4.0-fold significantly higher than AS25), and intermediate in AS11 (2.2-fold significantly higher than AS25), and no significant difference (p = 0.172) was observed in B2M1 expression between AS11 and AS26 (Fig. 14A). Similar to QPCR mRNA expression profiles of paralogues GAPDH1 and GAPDH2, the mRNA expression profile of putative paralogue B2M2 was different from that of B2M1, showing lowest expression in AS25, highest in AS11 (10.5-fold significantly higher than AS25), and intermediate in AS26 (8.5-fold significantly higher

than AS25), and no significant difference (p = 0.574) was observed in B2M2 expression between AS11 and AS26 (Fig. 14B).

FTM-like transcripts (GO:0008199, Ferric iron binding; GO:0016491, Oxidoreductase activity) were more highly expressed in two fast-growing Atlantic salmon families when compared with the slow-growing family in the microarray studies (Table 2; Appendices II and IV). QPCR mRNA expression of FTM in AS25 was significantly different from AS11 (2.1-fold higher than AS25) and AS26 (3.2-fold higher than AS25), and no significant difference (p = 0.210) was observed between AS11 and AS26 (Fig. 11D).

The mRNA expression of two SEPP putative paralogues (GO:0008430, Selenium binding) identified in GenBank as pseudogenes (SEPP1: BT072678; SEPP2: BT072221) was shown in the microarray study to be more highly expressed in at least one fast-growing family compared with the slow-growing family (Appendices II or IV). In the QPCR study, SEPP1 had the lowest mRNA expression in AS25, the highest in AS26 (2.8-fold significantly higher than AS25), and the intermediate expression in AS11 (1.7-fold not significantly higher than AS25; p = 0.098); no significant difference was detected between AS11 and AS26 (p = 0.114) (Fig. 15A). SEPP2 had a similar expression profile to SEPP1, showing the lowest mRNA expression level in family AS25, highest in AS26 (5.1-fold significantly higher than AS25), and intermediate expression in AS11 (2.9-fold significantly higher than AS25); no significant (p = 0.053) difference was observed between AS11 and AS26 (Fig. 15B).

For the two slow-growth associated transcripts from the microarray study selected for QPCR, AA5 (Appendix III) (GO:0005509, Calcium ion binding; GO:0005544,

Calcium-dependent phospholipid binding) and ADAMTS1 (Table 2; Appendices III and V) (GO:0004222, Metalloendopeptidase activity; GO:0008270, Zinc ion binding), the mRNA expression of neither transcript was validated as significantly more highly expressed in slow-growing families compared to either fast-growing family in the QPCR study (Fig. 11 F and G). In fact, ADAMTS-1 mRNA expression was shown by QPCR to be 2.4-fold significantly higher in fast-growing AS26 compared with slow-growing AS25 (Fig. 11F). AA5 showed non-significant slightly lower mRNA expression (1.1-fold) in fast-growing family AS11 compared with slow-growing family AS25 that agreed with microarray results in direction of change (Fig. 11G).

Since QPCR study was performed using biological replicates (i.e. RNA samples from individual fish), the RQ values of TOIs were compared between females and males in each family using two-sample t-test implemented in Minitab v15.1; no significant ($p > 0.05$) effects of sex on gene expression were observed (data not shown).

4. DISCUSSION

Triploid GH transgenic (3NGHTg) Atlantic salmon technology may enhance fish production by reducing the time required for animals to reach market size. As it was observed that growth performance of 3NGHTg Atlantic salmon varied among families (Fig. 1), the aim of this study was to identify and validate transcript expression correlates of enhanced growth performance of 3NGHTg fish using a functional genomics approach. Using the cGRASP 32K cDNA microarray platform (Koop et al., 2008), two microarray studies were carried out to compare the global constitutive hepatic transcript expression of two fast-growing families (AS11 and AS26) to a slow-growing family (AS25) of 3NGHTg Atlantic salmon (Fig. 4A). These two microarray studies gave rise to a total of 687 differentially expressed microarray informative features (more than two-fold expression differences in any three out of four technical replicates, with the same direction of change in the fourth technical replicate, and passing threshold in all four technical replicates in a given comparison) between fast-growing and slow-growing families of 3NGHTg Atlantic salmon (Appendices II-V) including 39 microarray features that were consistently expressed at higher levels in both fast-growing families and one microarray feature that was consistently expressed at a higher level in the slow-growing family compared with both fast-growing families (Fig. 4 B and C, Table 2). The GO term enrichment analysis of differentially expressed microarray features identified 35 GO terms significantly enriched in fast-growing or slow-growing 3NGHTg Atlantic salmon families (Table 3). In addition, six of these GO terms (glycolysis, peptidyl-cysteine S-

nitrosylation, lipoprotein metabolic process, oxygen transport, iron ion transport and homeostasis) were more frequently represented in a given list than expected by chance in fast-growing or slow-growing 3NGHTg salmon families in both comparisons (Table 3), suggesting these physiological processes may be associated with growth performance.

QPCR validation using individual samples (to assess biological variability) was conducted to analyze the expression of a subset of microarray-identified transcripts with annotations (i.e. not unknowns) that were consistently associated with growth performance. The QPCR results supported the microarray results in direction of change for 12 out of 13 fast-growth associated transcripts analyzed. The exception was NUPR1, where QPCR confirmed the microarray results in direction of change in the AS26 vs. AS25 comparison (2.2-fold non-significantly higher expression in family AS26 compared with AS25), but showed no difference in the comparison between AS11 and AS25 in the QPCR experiment (Fig. 11E). The two microarray-identified transcripts associated with slow growth (ADAMTS1 and AA5) were not validated by QPCR (Fig. 11 F and G). This discrepancy between microarray and QPCR results may be due to the presence of splice variants (e.g. AA5, see Table 4 footnotes for details) or the presence of unidentified paralogues or other related targets that could influence microarray results by non-specific hybridization to microarray probes. The growth-related transcripts identified and validated in the current study may guide the future development of genetic markers for the selection of broodstock that can be used to generate rapidly growing and reproductively sterile 3NGHTg Atlantic salmon. The emphasis of this study was placed on transcripts that were consistently associated with fast-growth in 3NGHTg Atlantic salmon (Table 2) as well as the biological processes (e.g. metabolism, iron homeostasis

and oxygen transport, and immune- and stress-related response) that are associated with these transcripts or their putative orthologues.

4.1 Carbohydrate metabolism

The liver is involved in a number of metabolic activities. Hepatocytes, which make up the majority of liver tissue, have been reported to regulate the level of glucose through several pathways (e.g. glycolysis and gluconeogenesis) in fish and mammals indicating an important role in glucose homeostasis (Blouin et al., 1977; Enes et al., 2009; Klover and Mooney, 2004). In a study of coho salmon, it was observed that GH transgenesis affected growth performance as transgenic fish preferentially used carbohydrate for energy production while shifting lipid and amino acid metabolism to more anabolic roles (Leggatt et al., 2009). Our analysis of the differences in the constitutive hepatic transcriptome of 3NGHTg salmon with different growth rates also revealed a number of fast-growth associated transcripts encoding key elements in various energetic metabolic pathways (i.e. carbohydrate, amino acid and lipid metabolism) (Table 2). For example, four putative fast-growth associated transcripts identified in this study encode enzymes involved in the glycolysis. They are three GAPDH paralogues and a transcript encoding 6-phosphofructokinase (PFK) (Table 2; Appendices II and IV, Fig. 13). GAPDH is known as a major glycolytic enzyme that converts glyceraldehyde-3-phosphate (G3P) to 1,3-diphosphoglycerate (1,3dPG) by oxidative phosphorylation (Sirover, 1999; Watson and Banaszak, 1964). Studies of mammals have shown that the expression of GAPDH can be affected by various metabolic conditions such as energy

deficiency as a result of fasting (Corbin et al., 2002; Rhoads et al., 2003). In addition, there is evidence that GAPDH plays a role in apoptosis and proliferation in dividing rat hepatocytes (C-9 rat cell line) in response to the elevated energy requirements associated with cell division (Barbini et al., 2007). Decrease in activity of PFK was observed in the liver of rainbow trout in response to high protein diet (Cowey et al., 1981) and fasting (Fideu et al., 1983). Recently, the activation of PFK was demonstrated to maintain glycolysis in HIF-1 deficient murine tumors (Golinska et al., 2011). These authors have all suggested that the increased PFK activity was a response to decrease glucose availability. Interestingly, genes involved in carbohydrate metabolism were highly up-regulated in liver of GH transgenic coho salmon relative to wild type salmon, and this result was also found in domesticated strains that exhibited enhanced growth rate when compared with wild type salmon (Devlin et al., 2009). In light of these previous studies, it is possible that the elevated expression of these transcripts involved in glycolysis observed in fast-growing 3NGHTg Atlantic salmon may be linked to the elevated carbohydrate metabolism.

4.2 Lipid metabolism

Lipid metabolism is another important aspect affecting somatic growth, and GH is known to affect the expression of several transcripts encoding proteins involved in lipid metabolism in salmonids (Gahr et al., 2008; Rise et al., 2006). In the current study, a total of five transcripts involved in lipid metabolism (APOAI, APOAIV, ACBP, D5DP, and

myelin basic protein) were identified by microarray as fast-growth associated transcripts in both 3NGHTg Atlantic salmon families (Table 2).

Two Atlantic salmon microarray features encoding an APOAI-2-like protein were found to be associated with enhanced growth in 3NGHTg salmon (Appendices II and IV). Using BLASTn of these microarray-identified sequences against the NCBI's nucleotide database, two APOAI-like paralogues, referred to as APOAI-1 (GenBank ID: BT049771) and APOAI-2 (GenBank ID: BT048392) were identified (Table 4; Appendices II and IV). Although no Atlantic salmon APOAI-1-representing microarray features were differentially expressed in the current study, one microarray feature representing a putative rainbow trout APOAI-1 paralogue was among the informative growth-associated transcripts of the current study (Appendix IV). In the current QPCR study, paralogue-specific primers were designed for APOAI-1 and APOAI-2; similar expression patterns were detected for these APOAI paralogues, both having higher expression in fast-growing families with the highest fold change found in the AS26 vs. AS25 comparison (Fig. 12). In mammals, APOAI is a key protein component of the high-density lipoproteins (HDLs) that play important roles in lipid metabolism and reverse transport of lipids (e.g. from storage in adipose tissues to tissues that use it for energy production like skeletal muscle) (Lewis and Rader, 2005). In study of teleost fish, APOAI was detected in hepatocytes of cod liver in all larval stages and in several organs where apoptosis occurred suggesting an important role of APOAI in the organogenesis and homeostasis in larval development (Lange et al., 2005). As a multifunctional protein, APOAI also displayed potent antimicrobial activities in common carp (*Cyprinus carpio* L.) and rainbow trout, showing high expression in the primary defence barrier (e.g. epidermis, gills, and intestinal

mucosa) and ability to inhibit growth of fish pathogens (Concha et al., 2004; Villarroel et al., 2007). Like the APOAI paralogues, APOA-IV was found in the current microarray and QPCR experiments to be more highly expressed in fast-growing 3NGHTg salmon families AS11 and AS26 in comparison to the slow-growing family (Table 2; Fig. 11B). In mammals, APOAIV is involved in the assembly of chylomicrons that deliver dietary lipid from liver to peripheral tissues, and it is also known to play a vital role in the regulation of food intake, particularly in intestinal lipid flux (Black, 2007). Interestingly, an increase in transcript expression of APOAIV was observed in muscle of slow-growing rainbow trout treated with exogenous GH (Gahr et al., 2008). Given the above, the association between high expression levels of apolipoprotein-encoding transcripts and fast-growth may be linked to the high lipid demand of somatic cells for fast growth.

A transcript coding for acyl-CoA-binding protein (ACBP) was more highly expressed in the fast-growing families relative to the slow-growing family in the microarray studies (Table 2; Appendices II and IV), and the direction of its mRNA expression response to fast growth was confirmed by QPCR (Fig. 11A). ACBP is a 10kDA protein that binds long chain acyl-CoA esters with very high affinity and specificity, and its function is highly conserved in different species from yeast to humans (Burton et al., 2005). In the fruit fly (*Drosophila melanogaster*), ACBP was detected at the mRNA level in most tissues that are associated with energy metabolism (Kolmer et al., 1994). ACBP has also been found in various tissues in rat at both protein and mRNA levels with the highest concentration in liver (Bovolin et al., 1990). Following ACBP silencing, growth arrest and cell death were observed in human cell lines (i.e. HeLa, HepG2, and Chang cells) (Faergeman and Knudsen, 2002). The depletion of ACBP in

yeast *Saccharomyces cerevisiae* reduced synthesis of very long-chain fatty acids and sphingolipids and caused alterations in membrane structure and organization (Gaigg et al., 2001). Recent studies suggested that ACBP regulates transcription of genes involved in phospholipid biosynthesis and fatty acid metabolism in yeast (Faergeman et al., 2007) and in human liver (Vock et al., 2010). Therefore, the elevated transcript expression of ACBP in fast-growing families of 3NGHTg salmon may indicate additional effects of lipid biosynthesis occurring in these fish.

Delta-5-desaturase protein (D5DP) and delta-6-desaturase protein (D6DP) catalyze the biosynthesis of eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), which are polyunsaturated omega-3 fatty acids that are essential for the health and development of fish (Copeman et al., 2002; Mazorra et al., 2003). In Atlantic salmon, D5DP and D6DP transcripts are expressed at high levels in intestine, liver and brain (Zheng et al., 2005), and their mRNA expression levels were induced by a decrease in dietary EPA and DHA (Monroig et al., 2010). Moreover, the mRNA expression of D6DP was induced in liver of GH transgenic coho salmon on a full ration compared to GH transgenic coho salmon on a restricted ration or non-transgenic coho salmon on full ration (Rise et al., 2006). In the current study, both D5DP- and D6DP-representing transcripts were microarray-identified as differentially expressed in fast-growing and slow-growing 3NGHTg salmon liver samples in at least one comparison (Appendix II or IV), however, only D5DP was expressed at higher levels in both fast-growing families of 3NGHTg salmon (Table 2, Fig. 11C). The higher expression of D5DP-encoding transcript observed in fast-growing 3NGHTg salmon families might serve to compensate for the high demand for EPA and DHA as a result of rapid growth. From an aquaculture perspective, not only

is the expression level of D5DP important for growth performance, it could also help to reduce the reliance on dietary EPA and DHA supplementation. The microinjection of the masu salmon (*Oncorhynchus masou*) D5DP gene into zebrafish embryos was shown to increase synthesis of EPA and DHA in the resulting adult zebrafish fed with poor live food (i.e. *Artemia* nauplii that have less EPA and no DHA compared to commercial feed) (Alimuddin et al., 2007), which would help to reduce the requirement of fish meal/oil content in feed formulation. Given the fact that D5DP-representing transcripts showed high transcript levels in fast-growing 3NGHTg salmon families in this study, fast-growing 3NGHTg Atlantic salmon strains with higher D5DP and D6DP transcript expression could not only benefit aquaculture industry by growing faster but could also potentially provide a superior nutritional product raised on a more sustainable feed source.

4.3 Amino acid metabolism

Previous studies of muscle, liver and intestine suggested that the fast growth achieved by GH transgenic coho salmon is partly due to their ability to deposit a higher percentage of dietary protein than their non-transgenic counterparts (Higgs et al., 2009; Raven et al., 2008). Nitrogen retention appears to be an important step in efficiently converting dietary protein to somatic growth as less ammonia excretion was observed in GH-transgenic Arctic char (*Salvelinus alpinus*) and Nile tilapia (*Oreochromis niloticus*) in comparison to their non-transgenic counterparts (Kobayashi et al., 2007; Pitkanen et al., 1999). Glutamine synthetase (GS) is a key enzyme in this process as it retrieves

nitrogen from ammonia, making it available to anabolic pathways in the form of glutamine. An increase in GS activity was observed in liver of transgenic coho salmon in comparison to their non-transgenic counterparts (Leggatt et al., 2009). Collectively, the identification of GS as a liver transcript associated with fast growth in both microarray comparisons in the current study (Appendices II and IV) may suggest a decrease in ammonia excretion and thus an increase in dietary protein deposition in fast-growing 3NGHTg salmon. Since it was observed that GAPDH transcription in human hepatocytes increased with the accumulation of glutamine (Claeyssens et al., 2003), it is possible that the higher transcript expression in GAPDH paralogues observed in fast-growing 3NGHTg salmon liver in the current study is linked to the increase in GS transcript expression as a result of increase in glycolytic flux in anabolic processes. Interestingly, our microarray studies also identified glutamate dehydrogenase (GDH) as a transcript more highly expressed in fast-growing families relative to a slow-growing 3NGHTg family (Table 2; Appendices II and IV). As part of the glutamate pathway, GDH is mainly expressed in perivenous hepatocytes and can be involved in both utilization and synthesis of glutamine (Reviewed in Watford, 2000). In the current study, the higher GS transcript expression combined with elevated GDH transcript expression observed in comparisons of fast-growing 3NGHTg salmon compared with slow-growing 3NGHTg salmon may collectively suggest an elevated glutamine synthesis in these fish, which may be the result of increased protein deposition required for rapid somatic growth.

4.4 Iron homeostasis and oxygen transport

The liver of vertebrates is an important organ for iron storage and metabolism (Reviewed in Graham et al., 2007), and ferritin is essential for the storage of intracellular iron. In hepatocytes, transferrin-bound iron that is circulated in plasma binds to transferrin receptors on the cell membrane surface and is taken up into cells by endocytosis. The non-transferrin-bound iron (NTBI) can be bound to serum proteins (e.g. albumin or citric acid). Within endosomes, ferric iron (Fe^{3+}) is converted to ferrous iron (Fe^{2+}) by enzymes of the six-transmembrane epithelial antigen of the prostate (STEAP) family and then transported to the cytoplasm for essential physiological reactions. The unused Fe^{2+} is stored in ferritin to prevent toxicity induced by iron overload (Kohgo et al., 2008; Takami and Sakaida, 2011). In the current microarray study, many transcripts encoding ferritin heavy (FTH) and ferritin middle (FTM) subunits were identified as having higher expression in fast-growing 3NGHTg Atlantic salmon liver (Table 2; Appendices II and IV), and the QPCR study further confirmed the higher transcript expression of FTM in fast-growing families of 3NGHTg salmon when compared to a slow-growing family (Fig. 11D). Consistent with higher expression observed for ferritin-encoding transcripts, higher expression for transcripts encoding transferrin and serum albumin in fast-growing 3NGHTg salmon families relative to a slow-growing family was also seen in the microarray study (Appendices II and IV). These results may suggest an altered iron ion homeostasis in these fish as transferrin and serum albumin both play important roles in iron transport and storage (Silva and Hider, 2009). Iron homeostasis and oxygen metabolism are closely linked processes as iron is involved in the redox reactions that

allow hemoglobin to transport oxygen (Theil, 2003). Our microarray results showed that the transcripts encoding several hemoglobin subunits were expressed at higher levels in fast-growing families compared to a slow-growing family (Table 2). Elevated hepatic transcript expression of hemoglobin subunits α and β were previously observed in GH transgenic coho salmon, which had enhanced growth rate in comparison to their non-transgenic counterparts (Rise et al., 2006). Given the role of hemoglobin in oxygen transport, it is reasonable to hypothesize that the elevated expression of hemoglobin-encoding transcripts in fast-growing fish observed in this study is a response of enhanced growth salmon to increased metabolic demands. However it is also possible that livers of fast-growing fish are more highly vascularized than those of slow-growing fish, which could lead to an increased number of circulating erythrocytes and consequently higher levels of hemoglobin transcripts (Rise et al., 2006).

4.5 Other hepatic transcripts associated with fast-growing 3NGHTg Atlantic salmon

In the current study, several microarray-identified fast-growth associated transcripts had immune- and stress-relevant functional annotations. Among those were: two beta-2-microglobulin (B2M) paralogues and major histocompatibility complex class I (MHC-I) (Table 2; Appendices II and IV; Fig. 14). B2M plays an important role in adaptive immune response to viral challenge in teleost. For example, B2M transcript expression is increased in the liver and head-kidney of infectious salmon anaemia virus (ISAV) injected Atlantic salmon (Jorgensen et al., 2006; LeBlanc et al., 2010) and in spleen and intestine of rainbow trout during infectious hematopoietic necrosis virus

(IHNV) infection (Hansen and La Patra, 2002). B2M is a light chain component of MHC class I complexes that expose antigenic peptides to cytotoxic T-cells and subsequently activate cellular immunity in the host for control of virus infections (York and Rock, 1996). Although it is known that MHC-I is involved in immune responses to viral pathogens, and considered to be a robust hepatic stress indicator in rainbow trout (Momoda et al., 2007), the potential roles of these immune-relevant proteins in somatic growth of salmonids remain to be studied. Nonetheless, the microarray results for the B2M paralogues were validated by the QPCR analysis, which indicates that these transcripts may be involved in enhanced growth. Similar to the GAPDH paralogues, these two B2M transcripts showed distinct expression profiles with B2M1 having the highest fold change in AS26 compared to AS25, while for B2M2 the highest fold change was seen in AS11. Differences in expression profiles between two paralogues might indicate functional differentiation of transcripts corresponding to duplicated genes.

Although SEPP1 and SEPP2 were identified as pseudogenes, they were observed in the current microarray and QPCR studies to be highly expressed at the mRNA level in one fast-growing family compared with the slow-growing family. In a previously published microarray study, mRNA expression of SEPP was shown to be highly repressed in *Piscirickettsia salmonis*-infected macrophages and head kidney in Atlantic salmon (Rise et al., 2004a). Further investigation is required to test whether SEPP1 and SEPP2 have molecular functions that are associated with growth performance, immune response or other unknown biological processes.

Five nuclear protein 1 (NUPR1)-like features were greater than two-fold more highly expressed in fast-growing 3NGHTg Atlantic salmon families compared with a

slow-growing family in the microarray studies (Appendices II and IV), and one NUPR1-like feature was consistently associated with fast-growth in both microarray comparisons (Table 2). However, QPCR analysis of individual RNA samples failed to confirm the microarray findings, showing no expression difference in one fast-versus-slow comparison (AS11 vs. AS25) but more than two-fold expression difference ($p = 0.074$) in the other fast-versus-slow comparison (AS26 vs. AS25) (Fig. 11E). Possible explanations for disagreement between microarray and QPCR results (e.g. unknown paralogues influencing microarray hybridization) have been presented previously. When a reference Atlantic salmon genome sequence is available (Davidson et al., 2010), it will be fairly straightforward to identify and develop specific QPCR assays for all putative paralogues for TOIs in functional genomics studies. NUPR1 was firstly identified as p8 in rat pancreatic acinar cells during the acute phase of pancreatitis, and its mRNA expression was detected in tissue cells in response to apoptosis and cell growth (Mallo et al., 1997). In mouse liver, NUPR1 depletion strongly altered the expression of genes involved in vital cellular pathways and its up-regulation after exposure to various stress agents (e.g. LPS and CCl_4) suggested the importance of this protein in cellular defence system (Taieb et al., 2005; Vasseur et al., 2003). A microarray study in rainbow trout liver reported NUPR1 transcript as a robust indicator of stress (Momoda et al., 2007). On the other hand, it was reported that expression of NUPR1 transcript was indirectly suppressed by somatic growth of GH transgenic coho salmon under different feeding strategies (Rise et al., 2006). Based on these findings, the induction of NUPR1 mRNA level in the current microarray study might suggest fast-growing 3NGHTg Atlantic salmon liver tissues experience cellular stress and nutrient deficits.

Two transcripts encoding histone subunits (H1.0 and 3.3) were greater than two-fold more highly expressed in fast-growing 3NGHTg Atlantic salmon compared with slow-growing salmon liver (Appendices II and IV). Human histone H1 has several variants that exhibited distinct functions in gene expression and cell growth (Sancho et al., 2008). In Atlantic salmon, H1 was found to be an antimicrobial protein in liver suggesting a role in innate immunity (Richards et al., 2001). Depressed regulation of normally highly expressed genes was detected in H3.3-deficient *Drosophila* when compared with *Drosophila* containing H3.3, suggesting that this protein is important for proper transcription of genes (Sakai et al., 2009). However, this result was not consistently shown in some studies and whether this histone variant is essential in active gene transcription is still under debate (Szenker et al., 2011). Interestingly, H2A histone family member Z and histone H5 transcripts were also shown by microarray to be more highly expressed in GH transgenic coho salmon liver compared to control non-transgenic coho salmon liver (Rise et al., 2006). It was previously proposed that modulation of histone-like transcript expression may be part of the mechanisms by which fast-growing fish liver cells control overall transcription in a high-proliferative state (Rise et al., 2006).

4.6 Conclusions

This study utilized DNA microarrays and QPCR to identify and validate hepatic transcripts that were differentially expressed between fast-growing and slow-growing 3NGHTg Atlantic salmon families. Many of the transcripts that were identified as more highly expressed in the fast-growing families compared with the slow-growing family are

hypothesized to be associated with increased metabolic rate. This study improved our understanding of the genes and molecular pathways involved in growth performance of 3NGHTg Atlantic salmon. The molecular biomarkers for fast-growing 3NGHTg Atlantic salmon that were identified and validated in this study may guide the future development of genetic markers for the selection of broodstock that can be used to generate rapidly growing, reproductively sterile 3NGHTg Atlantic salmon.

4.7 Future research

In this study, functional genomics approaches were used to identify and validate several growth-relevant transcripts in three 3NGHTg Atlantic salmon families. Further research (e.g. outlined in the next two paragraphs) will be needed to build on these results, with an ultimate goal of developing a set of molecular markers for selection of GHTg Atlantic salmon that show enhanced growth performance after induction of triploidy.

Among the six PIT-tagged experimental families in the current study, only one slow-growing 3NGHTg Atlantic salmon family was eligible for functional genomics analyses (see Materials and Methods for details). Future studies on growth-relevant transcript expression using additional fast-growing and slow-growing 3NGHTg Atlantic salmon families would improve the robustness and general applicability of the results.

In this study, many transcripts showed differences in level of expression in liver between fast-growing and slow-growing 3NGHTg Atlantic salmon families. Several of these transcripts, with functional annotations showing involvement in a number of

metabolic pathways, were considered to be candidate genes contributing to growth performance. Future structural (i.e. sequence) and transcript expression analyses of these growth-relevant genes (e.g. through RNA-seq-based transcriptome profiling) would identify SNPs that could be subjected to SNP genotyping with appropriate individuals to test for association between SNP markers and the fast-growth phenotype. Such association would suggest that there was a linked control of gene expression and SNPs that influence growth performance of 3NGHTg Atlantic salmon families.

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APPENDICES

APPENDIX I. Supplemental tables showing growth performance data of three triploid GH transgenic (3NGHTg) Atlantic salmon family (AS25, AS11, and AS26) over a period of approximately 45 days.

Appendix I. A. The initial and final weight of 3NGHTg Atlantic salmon family (AS25, AS11, and AS26).

Sample name	Initial weight (g)	Mean initial weight (g)	SE initial weight (g)	Final weight (g)	Mean final weight (g)	SE final weight (g)
AS25_153_F	68.4	64.5	3.5	114.7	115.1	4.1
AS25_154_F	57.4			106.2		
AS25_155_F	64.5			111.9		
AS25_156_M	83.3			133.8		
AS25_157_M	67.3			105.2		
AS25_159_F	59.8			118.5		
AS25_160_M	54.8			118.1		
AS25_164_F	75.6			131.9		
AS25_167_F	49.8			95.4		
AS11_151_F	23.2	39.1	3.4	61.9	97.2	7.7
AS11_155_F	43.9			98.5		
AS11_156_M	40.4			97.4		
AS11_158_F	25.7			74.0		
AS11_160_F	50.5			132.3		
AS11_161_M	48.2			104.5		
AS11_162_F	45.3			110.5		
AS11_166_M	45.2			121.1		
AS11_168_M	29.4			74.8		
AS26_252_F	23.4	46.1	3.2	77.9	109.2	6.4
AS26_253_F	43.9			87.2		
AS26_254_F	44.7			118.7		
AS26_256_M	51.3			115.1		

AS26_257_F	38.3		111.7
AS26_260_M	59.6		141.1
AS26_261_F	56.5		112.7
AS26_263_M	44.0		85.5
AS26_264_F	48.9		110.0
AS26_265_F	50.5		131.7

Appendix I. B. The initial and final length of 3NGHTg Atlantic salmon family (AS25, AS11, and AS26).

Sample name	Initial length (cm)	Mean initial length (cm)	SE initial length (cm)	Final length (cm)	Mean final length (cm)	SE final length (cm)
AS25_153_F	18.0	17.6	0.2	21.4	21.4	0.2
AS25_154_F	17.3			20.9		
AS25_155_F	17.7			21.9		
AS25_156_M	18.7			22.3		
AS25_157_M	17.9			20.3		
AS25_159_F	17.3			21.6		
AS25_160_M	17.2			21.5		
AS25_164_F	18.2			22.1		
AS25_167_F	16.3			20.4		
AS11_151_F	13.1	15.4	0.5	17.7	20.3	0.5
AS11_155_F	16.2			20.2		
AS11_156_M	15.9			20.7		
AS11_158_F	13.1			18.0		
AS11_160_F	16.7			22.4		
AS11_161_M	16.2			21.0		
AS11_162_F	16.5			21.3		
AS11_166_M	16.6			21.8		
AS11_168_M	14.2			19.2		
AS26_252_F	12.7	15.8	0.4	19.2	20.9	0.4

AS26_253_F	15.6		19.5
AS26_254_F	15.9		21.6
AS26_256_M	16.6		21.4
AS26_257_F	15.2		20.8
AS26_260_M	17.3		22.7
AS26_261_F	16.2		20.3
AS26_263_M	15.6		19.4
AS26_264_F	16.6		21.5
AS26_265_F	16.4		22.8

Appendix I. C. The weight-specific growth rate (SGR_W) of 3NGHTg Atlantic salmon family (AS25, AS11, and AS26).

Sample name	SGR_W	Mean SGR_W	SE SGR_W
AS25_153_F	1.20	1.37	0.08
AS25_154_F	1.46		
AS25_155_F	1.28		
AS25_156_M	1.10		
AS25_157_M	1.06		
AS25_159_F	1.59		
AS25_160_M	1.83		
AS25_164_F	1.29		
AS25_167_F	1.51		
AS11_151_F	2.23	2.06	0.07
AS11_155_F	1.80		
AS11_156_M	1.96		
AS11_158_F	2.35		
AS11_160_F	2.19		
AS11_161_M	1.72		
AS11_162_F	1.98		
AS11_166_M	2.24		

AS11_168_M	2.08		
AS26_252_F	2.67	1.95	0.13
AS26_253_F	1.53		
AS26_254_F	2.22		
AS26_256_M	1.80		
AS26_257_F	2.43		
AS26_260_M	1.96		
AS26_261_F	1.53		
AS26_263_M	1.48		
AS26_264_F	1.80		
AS26_265_F	2.13		

Appendix I. D. The length-specific growth rate (SGR_L) of 3NGHTg Atlantic salmon family (AS25, AS11, and AS26).

Sample name	SGR_L	Mean SGR_L	SE SGR_L
AS25_153_F	0.40	0.45	0.02
AS25_154_F	0.45		
AS25_155_F	0.50		
AS25_156_M	0.41		
AS25_157_M	0.30		
AS25_159_F	0.52		
AS25_160_M	0.53		
AS25_164_F	0.45		
AS25_167_F	0.52		
AS11_151_F	0.68	0.62	0.02
AS11_155_F	0.49		
AS11_156_M	0.59		
AS11_158_F	0.71		
AS11_160_F	0.67		

AS11_161_M	0.58		
AS11_162_F	0.57		
AS11_166_M	0.62		
AS11_168_M	0.67		
AS26_252_F	0.92	0.63	0.04
AS26_253_F	0.50		
AS26_254_F	0.70		
AS26_256_M	0.56		
AS26_257_F	0.71		
AS26_260_M	0.62		
AS26_261_F	0.50		
AS26_263_M	0.48		
AS26_264_F	0.57		
AS26_265_F	0.73		

APPENDIX II. Supplemental table containing 116 transcripts with greater than 2-fold higher expression in triploid growth hormone transgenic (3NGHTg) Atlantic salmon family AS11 (fast-growing) in comparison to 3NGHTg Atlantic salmon family AS25 (slow-growing) in any 3 out of 4 technical replicate microarrays including at least one dye-swap.

EST[1]	Gene Name of Best BLASTX or BLASTN [(N)] Hit[1]	Length (% ID)[1]	E value[1]	Function of Best BLAST Hit[2]	$\overline{X}$ Fold Change[3]	SEM[3]
CA042535	40 kDa peptidyl-prolyl cis-trans isomerase [ACO07506; *Oncorhynchus mykiss*]	103 (100%)	7E-47	Binding; Peptidyl-prolyl cis-trans isomerase activity (GO:0005488; GO:0003755) [C1BEQ3]	2.277	0.207
CB492405	40S ribosomal protein S11 [ACO15454; *Caligus clemensi*]	105 (100%)	3E-54	Structural constituent of ribosome (GO:0003735) [C1C2F1]	2.781	0.149
CB491393	40S ribosomal protein S13 [ACO08029; *Oncorhynchus mykiss*]	139 (99%)	9E-73	Structural constituent of ribosome (GO:0003735) [C1BG76]	2.903	0.309
CB492978	40S ribosomal protein S27 [ABJ98653; *Psetta maxima*]	87 (98%)	1E-37	Metal ion binding; Structural constituent of ribosome (GO:0046872; GO:0003735) [A0EZY9]	2.251	0.273
CB486904	40S ribosomal protein S3 [ACI67079; *Salmo salar*]	137 (100%)	7E-71	RNA binding; Structural constituent of ribosome (GO:0003723; GO:0003735) [B5X8A9]	2.428	0.242
CA042530	6-phosphofructokinase, liver type [AAI26579; *Bos taurus*]	199 (78%)	9E-87	6-phosphofructokinase activity; ATP binding; Metal ion binding (GO:0003872; GO:0005524; GO:0046872) [A1A4J1]	2.867	0.544
CB493831	60S ribosomal protein L13 [ACN10300; *Salmo salar*]	27 (100%)	5E-9	Structural constituent of ribosome (GO:0003735) [C0H8D1]	4.028	1.242

CB493696	Acyl-CoA-binding protein [ACI68322; *Salmo salar*] (ACBP, Fig. 11A)	42 (95%)	9E-16	Fatty-acyl-CoA binding (GO:0000062) [B5XBV2]	3.021	0.587
CA041892	Apolipoprotein A-I precursor [ACI68193; *Salmo salar*] (*Salmo salar* type 2) (APOAI-2, Fig. 12B)	44 (100%)	5E-16	Lipid binding (GO:0008289) [B5XBH3]	3.444	0.709
CB496971	Apolipoprotein A-I-2 [AAB96973; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	54 (100%)	5E-14	Lipid binding (GO:0008289) [O57524]	3.201	0.288
CB493958	Apolipoprotein A-IV precursor [ACI67266; *Salmo salar*] (APOAIV, Fig. 11B)	121 (98%)	3E-57	Lipid binding (GO:0008289) [B5X8U6]	2.509	0.381
CB496646	Apolipoprotein B [ACO82023; *Perca flavescens*] (*Oncorhynchus mykiss* feature)	116 (40%)	5E-20	Unknown	2.533	0.588
CA042402	Apolipoprotein B 100 (Mutant) [ADN03360; *Homo sapiens*]/[EZ905147; *Oncorhynchus mykiss*] (B) (X) (*Salmo salar* feature)	289 (34%)/ 143 (97%)	1E-35/ 8E-59	Lipid transporter activity (GO:0005319) [E1A689]	4.430	0.636
CB497208	ATP synthase subunit epsilon, mitochondrial [ACI68480; *Salmo salar*]	52 (100%)	3E-20	Hydrogen ion transporting ATP synthase activity, Rotational mechanism; Proton-transporting ATPase activity, Rotational mechanism (GO:0046933; GO:0046961) [B5XCB0]	2.188	0.236
CA054842	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 [ACH70848; *Salmo salar*]	192 (99%)	1E-102	Hydrogen ion transmembrane transporter activity (GO:0015078) [B5DGH4]	3.220	0.688
CB505594	Beta-2 microglobulin [AF180486; *Salmo salar*] (N) (*Salmo salar*	799 (99%)	0	MHC class I protein complex	2.248	0.259

	type 1) (B2M1, Fig. 14A)			(GO:0042612) [Q9DG62] [c]		
CB505897	Beta-2 microglobulin type 2 [AAP51056; *Oncorhynchus mykiss*] (*Salmo salar* type 2) (B2M2, Fig. 14B)	24 (92%)	2E-12	MHC class I protein complex (GO:0042612) [Q6XQ10] [c]	3.400	0.396
CA043324	Beta-2-microglobulin precursor [BT047559; *Salmo salar*] [(N)] (*Salmo salar* type 2) (B2M2, Fig. 14B)	542 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DD81] [c]	3.004	0.485
CA061048	Beta-2-microglobulin precursor [BT047559; *Salmo salar*] [(N)] (*Salmo salar* type 2) (B2M2, Fig. 14B)	608 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DD81] [c]	3.906	0.453
CK990806	Beta-2-microglobulin precursor [BT056667; *Salmo salar*] [(N)] (*Salmo salar* type 2) (B2M2, Fig. 14B)	165 (98%)	2E-74	MHC class I protein complex (GO:0042612) [B9ELZ2] [c]	3.971	1.052
CK990545	Beta-2-microglobulin precursor [BT057038; *Salmo salar*] [(N)] (*Salmo salar* type 3)	445 (91%)	2E-169	MHC class I protein complex (GO:0042612) [B5XE24] [c]	2.422	0.304
CK991314	Beta-2-microglobulin precursor [BT074080; *Oncorhynchus mykiss*] [(N)] (*Oncorhynchus mykiss* feature)	509 (97%)	0	MHC class I protein complex (GO:0042612) [C1BHK1] [c]	2.234	0.127
CA051169	Betaine-homocysteine methyltransferase [ACH70821; *Salmo salar*]/[EZ763914; *Oncorhynchus mykiss*] [(B)]	95 (69%)/ 486 (92%)	4E-27/0	Betaine-homocysteine S-methyltransferase activity; Homocysteine S-methyltransferase activity; Zinc ion binding (GO:0047150; GO:0008898;GO:0008270) [B5DGE7]	3.318	0.201
CA059976	Brain protein 44-like protein, isoform CRA_a [EDL02117; *Mus musculus*] [(X)]	83 (86%)	8E-36	Mitochondrial inner membrane (GO:0005743) [D3Z5S0] [c]	2.663	0.453

CB494647	C-C motif chemokine 20 precursor [ACI66945; *Salmo salar*]	76 (91%)	2E-33	Chemokine activity (GO:0008009) [B5X7X5]	2.805	0.213
CA042390	Claudin-15 [ADO28272; *Ictalurus furcatus*]	133 (57%)	4E-35	Structural molecule activity (GO:0005198) [E3TD86]	2.829	0.353
CA050110	Cold-inducible RNA-binding protein [BT058753; *Salmo salar*] (N)	647 (99%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [C0H8U7]	2.535	0.227
CX142820	Complement component 1, q subcomponent-like 4 [AAI10813; *Homo sapiens*] (X)	141 (36%)	1E-13	Extracellular region (GO:0005576) [Q86Z23] [c]	2.851	0.305
CB493595	Delta5-desaturase-like protein [ABU87822; *Oncorhynchus masou*] (D5DP, Fig. 11C)	87 (99%)	2E-45	Heme binding; Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [A7XUS7]	3.681	0.615
CB512539	Digestive cysteine proteinase 2 precursor [ACI34170; *Salmo salar*]	185 (100%)	4E-108	Cysteine-type endopeptidase activity (GO:0004197) [B5X4D9]	2.378	0.571
CB496981	DNA-directed RNA polymerases I, II, and III subunit RPABC2 [ACO13758; *Esox lucius*]	56 (98%)	4E-24	DNA binding; DNA-directed RNA polymerase activity (GO:0003677; GO:0003899) [C1BXK5]	1.944	0.241
CA060826	Elongation factor 1-alpha 1 [ACN11490; Salmo salar] (*Salmo salar* feature)	38 (100%)	2E-11	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	5.221	1.319
DY733552	Elongation factor 1-alpha 1 [BT059777; *Salmo salar*] (N) (*Salmo salar* feature)	628 (100%)	0	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	2.697	0.628
DY711246	Extracellular matrix protein 1 precursor [BT059193; *Salmo salar*] (N)	640 (83%)	7E-149	Cellular Component: Extracellular space (GO:0005615) [C0HA37]	2.221	0.371

CB493178	Ferritin-H subunit [AAK08117|AF338763; *Oncorhynchus nerka*]	65 (95%)	8E-57	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [Q98TT0]	2.713	0.63
CB506201	Ferritin, middle subunit [ACI33572; *Salmo salar*] (*Salmo salar* feature) (Fig. 11D)	106 (100%)	7E-56	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5X2P1]	2.743	0.711
CB487639	Ferritin, middle subunit [ACI66713; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	130 (95%)	1E-66	Ferric iron binding (GO:0008199) [B5X793]	2.474	0.463
CB503780	Ferritin, middle subunit [ACI68639; *Salmo salar*] (*Salmo salar* feature)	162 (100%)	4E-89	Ferric iron binding (GO:0008199) [B5XCR9]	2.151	0.263
CB510731	Ferritin, middle subunit [ACO07744; *Oncorhynchus mykiss*] (*Salmo salar* feature) (Fig. 11D)	124 (100%)	3E-66	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [C1BFE1]	2.182	0.369
CA052094	Fructose-1,6-bisphosphatase [EU853449; *Salmo marmoratus*] (N)	65 (94%)	3E-17	Phosphoric ester hydrolase activity (GO:0042578) [B5AJU4]	3.024	0.546
CB514539	Fumarylacetoacetase [ACO09168; *Osmerus mordax*]	171 (87%)	1E-87	Fumarylacetoacetase activity (GO:0004334) [C1BJG5]	2.540	0.375
CA054111	Gamma-aminobutyric acid receptor-associated protein-like 2 [ACI66147; *Salmo salar*]	78 (100%)	6E-37	Receptor activity (GO:0004872) [B5X5M7]	2.543	0.384
CA053189	Glutamate dehydrogenase 1, mitochondrial precursor [BT044837; *Salmo salar*] (N)	515 (100%)	0	Binding; Oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor (GO:0005488; GO:0016639) [B5X1B8]	2.595	0.555
CB514092	Glutamine synthetase [ACI68482; *Salmo salar*] (*Salmo salar* feature)	27 (100%)	4E-8	ATP binding; Glutamate-ammonia ligase activity (GO:0005524; GO:0004356) [B5XCB2]	3.244	0.478
CB517817	Glutamine synthetase [ACI68482;	99 (100%)	5E-52	ATP binding; Glutamate-ammonia ligase	5.065	0.934

	Salmo salar] (*Salmo salar* feature)			activity (GO:0005524; GO:0004356) [B5XCB2]		
CB497579	Glutathione S-transferase [BAA76974; *Oncorhynchus nerka*]	159 (97%)	3E-84	Glutathione transferase activity (GO:0004364) [Q9W647]	2.460	0.277
CB492813	Glyceraldehyde-3-phosphate dehydrogenase [ACI33883; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	113 (100%)	5E-54	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X3K2]	3.564	0.76
CB498361	Glyceraldehyde-3-phosphate dehydrogenase [ACI66269; *Salmo salar*] (*Oncorhynchus mykiss* type 2)	146 (99%)	5E-78	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X5Z9]	2.308	0.254
CB510408	Glyceraldehyde-3-phosphate dehydrogenase [ACI66269; *Salmo salar*] (*Salmo salar* type 1) (GAPDH1, Fig. 13A)	183 (100%)	2E-100	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X5Z9]	2.733	0.761
BU965756	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*] (*Salmo salar* type 2) (GAPDH2, Fig. 13B)	116 (100%)	5E-60	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]	3.566	0.607
CB514460	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*] (*Salmo salar* type 2) (GAPDH2, Fig. 13B)	200 (100%)	2E-110	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]	3.940	1.272
CA039027	Glyceraldehyde-3-phosphate dehydrogenase-2 [ACH70939; *Salmo salar*]	64 (100%)	1E-29	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5DGR5]	5.119	0.772
DW584490	Heat shock 70 kDa protein [ACI34374; *Salmo salar*] (*Salmo salar* feature)	126 (99%)	4E-66	ATP binding (GO:0005524) [B5X4Z3]	2.460	0.211

CB485951	Heat shock cognate 70 kDa protein [AAB21658; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	182 (100%)	5E-99	ATP binding (GO:0005524) [P08108]	5.037	1.004
CB501216	Hemoglobin subunit alpha [ACI69100; *Salmo salar*] (*Salmo salar* type 1)	143 (100%)	5E-75	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XE30]	2.293	0.124
CB497564	Hemoglobin subunit alpha [ACI69100; *Salmo salar*] (*Salmo salar* type 1)	143 (99%)	9E-74	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XE30]	3.085	0.649
CA060701	Hemoglobin subunit alpha [ACN10007; *Salmo salar*] (*Salmo salar* type 2)	143 (100%)	1E-75	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H7I8]	3.832	1.693
CA064277	Hemoglobin subunit alpha [ACN10007; *Salmo salar*] (*Salmo salar* type 2)	143 (99%)	1E-75	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H7I8]	3.024	0.864
CB498419	Hemoglobin subunit alpha-1 [ACO07570; *Oncorhynchus mykiss*]	143 (100%)	8E-76	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [Q98974]	2.566	0.424
CA049318	Hemoglobin subunit alpha-4 [ACI66666; *Salmo salar*] (*Salmo salar* type 1) (*Salmo salar* type 1)	142 (100%)	5E-75	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5X746]	3.882	0.837
CB516893	Hemoglobin subunit alpha-4 [ACN09908; *Salmo salar*] (*Salmo salar* type 2) (*Salmo salar* type 2)	71 (99%)	2E-54	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H789]	3.178	0.550
FC072797	Hemoglobin subunit beta [ACI68762; *Salmo salar*] (*Salmo salar* feature)	94 (90%)	4E-38	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XD42]	2.667	0.540
CB496604	Hemoglobin subunit beta [ACO07479; *Oncorhynchus*	148 (100%)	5E-80	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037;	3.565	1.225

	mykiss] (*Oncorhynchus mykiss* feature)			GO:0019825; GO:0005344) [C1BEM6]		
DY729582	Hemoglobin subunit beta-1 [ACN09863; *Salmo salar*] (*Salmo salar* type 2)	131 (69%)	2E-40	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H744]	2.553	0.374
CA041804	Hemoglobin subunit beta-1 [ACN10193; *Salmo salar*] (*Salmo salar* type 1)	143 (98%)	3E-77	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H824]	2.182	0.359
CB497335	Hemoglobin subunit beta-1 [ACN10193; *Salmo salar*] (*Salmo salar* type 1)	157 (96%)	2E-82	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H824]	3.089	0.699
CB497309	Hemoglobin subunit beta-4 [ACO07576; *Oncorhynchus mykiss*]	148 (100%)	6E-80	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BEX3]	3.378	0.801
CB497659	Heparin cofactor II [AAN71003|AF515273; *Danio rerio*]/[EZ764595; *Oncorhynchus mykiss*] (B) (X)	304 (80%)/ 571 (99%)	1E-174/0	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q8AYE2]	3.034	0.697
CB497954	Histone H3.3 [BT057095; *Salmo salar*] (N)	684 (93%)	0	DNA binding (GO:0003677) [B5DG71]	2.226	0.304
CB496983	Homeobox protein PRH [ACO08286; *Oncorhynchus mykiss*]	137 (99%)	5E-66	Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity; Transcription regulator activity (GO:0043565; GO:0003700; GO:0030528) [C1BGY3]	2.177	0.221
CB498181	Kelch repeat and BTB (POZ) domain containing 10 [ACH70794; *Salmo salar*]	76 (96%)	5E-35	Unknown	2.338	0.051
CB493926	Keratin 18, simple type I keratin [CAA74664; Oncorhynchus mykiss]	73 (100%)	5E-24	Structural molecule activity (GO:0005198) [O57607]	3.054	0.678

CB496780	Kif1-binding protein [ABW89743; *Danio rerio*]	67 (73%)	2E-10	Binding (GO:0005488) [A8WE67]	2.714	0.424
EG925336	Kruppel-related zinc finger protein [AAC51180; *Homo sapiens*]	85 (45%)	3E-15	DNA binding; Zinc ion binding (GO:0003677; GO:0008270) [Q99676]	7.096	1.515
CB492896	McKusick-Kaufman syndrome, isoform CRA_a [EAX10343; *Homo sapiens*]	46 (52%)	5E-6	Protein binding (GO:0005515) [Q9HB66]	2.141	0.233
CB494688	Methyltransferase like 11B [AAI57907; *Mus musculus*]	48 (52%)	1E-5	Methyltransferase activity (GO:0008168) [B2RXM4]	2.597	0.533
CA048859	MHC Class I (Sasa-UBA) [EF210363; *Salmo salar*] (N)	566 (99%)	0	MHC class I protein complex (GO:0042612) [A7KDZ8] c	2.554	0.38
CK990992	Mitochondrial fission 1 protein [BT072691; *Salmo salar*] (N)	446 (97%)	0	Binding (GO:0005488) [C0PUR7]	2.369	0.2
CB498304	Mitochondrial inner membrane protein [ACI33218; *Salmo salar*]	43 (98%)	1E-14	Integral to mitochondrial inner membrane (GO:0031305) [B5X1N7] c	2.932	0.559
CB497206	Myelin basic protein [AAW52552; Danio rerio]/[EZ764180; *Oncorhynchus mykiss*] (B)	89 (44%)/ 44(100%)	1E-05/ 4E-12	Structural constituent of myelin sheath (GO:0019911) [Q5I2C7]	3.430	1.040
CB492886	N-terminal acetyltransferase complex ARD1 subunit homolog A [ACM09230; *Salmo salar*]	80 (95%)	1E-35	N-acetyltransferase activity (GO:0008080) [B9ENY3]	3.002	0.197
CA061418	Novel protein containing a vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain [CAK04616; *Danio rerio*]	214(66%)	2E-71	Calcium ion binding (GO:0005509) [Q1LY06]	3.105	0.423
CB515443	Nuclear autoantigenic sperm protein (histone-binding)	226 (68%)	3E-68	Binding (GO:0005488) [Q7ZVH7]	2.982	0.266

	[AAH45857; *Danio rerio*]					
CB490586	Nuclear protein 1 [AAH02109; *Mus musculus*] [X] (NUPR1, Fig. 11E)	57 (56%)	4E-11	Nucleus (GO:0005634) [Q9WTK0] [c]	4.604	1.081
CA061586	Nuclear receptor coactivator GT198 [AAL33609|AF440240; *Homo sapiens*] [X]	112 (67%)	1E-38	DNA binding (GO:0003677) [Q9P2W1]	2.393	0.136
CB501298	Pancreatic secretory trypsin inhibitor [ACM09634; *Salmo salar*]	67 (100%)	2E-36	Serine-type endopeptidase inhibitor activity (GO:0004867) [B9EQ37]	2.729	0.561
CB499048	Phosphatidylinositol-specific phospholipase C, X domain containing 1 [CAI43217; *Homo sapiens*]	71 (45%)	1E-9	Phospholipase C activity (GO:0004629) [Q9NUJ7]	2.273	0.437
DY736158	Plakophilin 4 protein [AAH82578; *Mus musculus*] [G]	1147 (74%)	2E-115	Binding (GO:0005488) [Q68FH0]	2.269	0.307
CB509563	Pre-mRNA-splicing factor 18 [ACO09138; *Osmerus mordax*]/[EZ871571; *Oncorhynchus mykiss*] [B]	247 (55%)/ 513 (88%)	3E-86/ 3E-161	Spliceosomal complex (GO:0005681) [C1BJD5] [c]	2.627	0.502
CA044554	Prothymosin, alpha a [AAH68334; *Danio rerio*] [X] (*Salmo salar* type 1)	36 (89%)	4E-8	Nucleus (GO:0005634) [Q6NV32] [c]	2.270	0.106
CA059252	Prothymosin, alpha a [BC068334; *Danio rerio*] [N] [X] (*Salmo salar* type 2)	194 (95%)	8E-78	Nucleus (GO:0005634) [Q6NV32] [c]	2.162	0.132
DY696044	RAS guanyl-releasing protein 2 [BT044818; *Salmo salar*] [N]	65 (89%)	3E-12	Guanyl-nucleotide exchange factor activity; Calcium ion binding (GO:0005085; GO:0005509) [B5X199]	4.256	1.218
CA054079	Retinol dehydrogenase 3 [ACI67927; *Salmo salar*]	191 (92%)	2E-98	Binding; Oxidoreductase activity (GO:0005488; GO:0016491) [B5XAQ7]	1.968	0.240

CA038814	Reverse transcriptase [AAS83200; *Fundulus heteroclitus*]	115 (29%)	1E-8	RNA binding; RNA-directed DNA polymerase activity (GO:0003723; GO:0003964) [Q64IX6]	6.337	1.423
CB509453	Ribosomal protein L3-like [ACH70797; *Salmo salar*]	169 (100%)	4E-96	Structural constituent of ribosome (GO:0003735) [B5DGC3]	4.673	1.298
CA040124	Selenoprotein P, plasma, 1a [AAI55822; *Danio rerio*]/[BT072678; *Salmo salar*] [(B)] (SEPP1, Fig. 15A)	169 (58%)/ 730 (99%)	2E-49/0	Selenium binding (GO:0008430) [A9JRW5]	3.761	1.111
CB505935	Selenoprotein P, plasma, 1a [AAI55822; *Danio rerio*]/[BT072678; *Salmo salar*] [(B)] (SEPP1, Fig. 15A)	169 (58%)/ 730 (99%)	2E-49/0	Selenium binding (GO:0008430) [A9JRW5]	3.254	0.921
CA063409	Serine/threonine-protein phosphatase PP1-beta catalytic subunit putative mRNA [BT072371; *Salmo salar*] [(N)]	623 (100%)	0	Phosphoprotein phosphatase activity (GO:0004721) [C0PUG4]	2.262	0.268
EG910863	Serum albumin 2 [CAA43187; *Salmo salar*]	232 (78%)	1E-96	Lipid binding; Metal ion binding (GO:0008289; GO:0046872) [Q03156]	4.331	1.169
CA063647	SET and MYND domain-containing protein 3 [ACI34045; *Salmo salar*]	153 (100%)	6E-87	Zinc ion binding (GO:0008270) [B5X414]	2.376	0.457
CB517445	Short chain dehydrogenase/reductase family 16C, member 5 [AAH54138; *Danio rerio*]/[EZ765850; *Oncorhynchus mykiss*] [(B) (X)]	298 (74%)/ 582 (89%)	4E-129/0	Binding; oxidoreductase activity (GO:0005488; GO:0016491) [Q7SZ49]	3.185	0.548
CA050950	Signal transducer/activator of transcription Stat1 [AAB60924; *Gallus gallus*] [(G)]	754 (68%)	2E-101	Calcium ion binding; protein binding; Sequence-specific DNA binding transcription factor activity; Signal transducer activity (GO:0005509; GO:0005515; GO:0003700;	2.117	0.116

				GO:0004871) [O13131]		
DY696917	Sulfatase modifying factor 2 [BT045086; *Salmo salar*] [(N)]	166 (87%)	1E-41	Binding (GO:0005488) [B5X217]	2.431	0.210
CK991342	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	50 (84%)	4E-19	Unknown	3.101	0.404
CA038301	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*] (*Salmo salar* feature)	76 (89%)	2E-30	Unknown	3.891	1.074
EG760655	Transposable element Tcb1 transposase [ACN11391; *Salmo salar*] (*Salmo salar* type 1)	68 (78%)	8E-23	Unknown	2.056	0.217
EG898809	Transposase [CAB51372; *Pleuronectes platessa*] (*Salmo salar* type 1)	181 (43%)	5E-25	Sigma factor activity; Sequence-specific DNA binding transcription factor activity; Transposase activity; DNA binding (GO:0016987; GO:0003700; GO:0004803; GO:0003677) [Q9PW00]	2.150	0.314
CA053140	Transposase [CAB51372; *Pleuronectes platessa*]/[BT072334; *Salmo salar*] [(B)] (*Salmo salar* type 2)	142 (38%)/ 448 (79%)	3E-15/ 3E-63	DNA binding; Sequence-specific DNA binding transcription factor activity; Sigma factor activity; Transposase activity (GO:0003677; GO:0003700; GO:0016987; GO:0004803) [Q9PW00]	2.040	0.301
CX245969	Tryptophan 2,3-dioxygenase [AAI51921; *Danio rerio*]	238 (83%)	2E-103	Iron ion binding; Tryptophan 2,3-dioxygenase activity (GO:0005506; GO:0004833) [A7MBU6]	2.567	0.345
CB490426	Ubiquitin-conjugating enzyme E2 T [ACM09373; *Salmo salar*]	133 (98%)	3E-71	Small conjugating protein ligase activity (GO:0019787) [B9EPC6]	3.315	0.83
CA044829	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.343	0.357
CA051002	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.302	1.122

CA051324	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.598	0.207
CA053709	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.517	0.456
CB509472	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.815	1.101
CB503374	Unknown (no significant BLAST hits)	NA	NA	Unknown	4.596	0.772

[1]Expressed sequence tags (EST) were identified by gene name of best BLASTX or BLASTN hit (lowest E value < 1e-05) from nucleotide or protein database. The length of aligned region, percent identity over aligned region and associated E value were presented. (N) For best BLASTN hits with informative gene name (NCBI); (B) For best BLASTX results of the best BLASTN hit (NCBI) if best BLASTX or N hits were not applicable, presented in "gene name [BLASTX results]/[BLASTN results]" format; (G) For BLAST results from cGRASP EST database (raw); (X) For best BLAST hits from *Homo sapiens*, *Mus musculus* or *Danio rerio* in BLAST results (NCBI), listed only if functional annotation of best BLASTX hit were not available. For features of same BLAST results, only *Salmo salar* features were processed with bioinfomatics in MegAlign software and manually assigned as "*Salmo salar* type #" (if more than one type applicable) or " Salmo salar feature " (only one type applicable) following their gene names.

[2]Function of the best BLASTX or BLASTN hit was interpreted as Gene Ontology (GO) in Swiss-Port protein knowledgebase following priority of molecular function, cellular component [c], and biological process [b].

[3]Mean fold changes and standard errors of mean were calculated based on normalized data from GeneSpring software (Agilent Technologies).

APPENDIX III. Supplemental table containing 27 transcripts with greater than 2-fold higher expression in triploid growth hormone transgenic (3NGHTg) Atlantic salmon family AS25 (slow-growing) in comparison to 3NGHTg Atlantic salmon family AS11 (fast-growing) in any 3 out of 4 technical replicate microarrays including at least one dye-swap.

EST	Gene Name of Best BLASTX or BLASTN [(N)] Hit	Length (% ID)	E value	Function of Best BLAST Hit	$\overline{X}$ Fold Change	SEM
CK990279	ADAMTS-1 protein [BAE16358; *Oryzias latipes*] (ADAMTS1, Fig. 11F)	148 (72%)	1E-58	Metalloendopeptidase activity; Zinc ion binding (GO:0004222; GO:0008270) [Q4AED3]	2.684	0.527
CB509241	Annexin A5 [ACN10184; *Salmo salar*] (AA5, Fig. 11G)	118 (97%)	6E-57	Calcium ion binding; Calcium-dependent phospholipid binding (GO:0005509; GO:0005544) [C0H815]	2.327	0.227
EG940879	ARMET protein [AAH07282; *Homo sapiens*] [(G) (X)]	182 (65%)	9E-57	Growth factor activity (GO:0008083) [P55145]	2.624	0.706
DW566612	Class I histocompatibility antigen [BT059396; *Salmo salar*] [(N)]	291 (85%)	1E-71	MHC class I protein complex (GO:0042612) [C0HAP0] [c]	2.490	0.512
EG771466	Digestive cysteine proteinase 2 precursor [ACI69888; *Salmo salar*]	224 (99%)	2E-128	Cysteine-type endopeptidase activity (GO:0004197) [B5XGB8]	2.847	0.569
CK991075	Gamma-glutamyl hydrolase precursor [ACI66462; *Salmo salar*]	149 (83%)	2E-66	Omega peptidase activity (GO:0008242) [B5X6J2]	4.157	1.005
EG928757	Golgin B1 [BAG48317; *Homo sapiens*] [(X)]	144 (48%)	2E-31	Golgi apparatus (GO:0005794) [B2ZZ91] [c]	2.123	0.107
CB502864	Hydroxyacid oxidase 1 [ACN10394; *Salmo salar*]	137 (100%)	4E-70	FMN binding; Oxidoreductase activity (GO:0010181; GO:0016491) [C0H8M5]	2.918	0.401
DW568458	Leucine rich repeat neuronal 3	279 (71%)	9E-113	Protein binding (GO:0005515) [Q9H3W5]	3.050	0.541

	[AAH35133; *Homo sapiens*]					
CB509058	Melanoma differentiation associated gene 5 [CAZ27715; *Oncorhynchus mykiss*]/[EZ764472;*Oncorhynchus mykiss*] [(B)]	207 (98%)/ 369 (85%)	1E-103/ 5E-95	ATP binding; ATP-dependent helicase activity; nucleic acid binding (GO:0005524; GO:0008026; GO:0003676) [D7F7W8]	2.384	0.293
CA053452	MHC class IA core region [HM210571; *Oncorhynchus mykiss*] [(N)]	193 (91%)	3E-63	MHC class I protein complex (GO:0042612) [Q9TNN8] [c]	2.370	0.395
CB517750	MHC class II antigen beta chain [EU008541; *Salmo salar*] [(N)]	234 (90%)	4E-77	MHC class II protein complex; Integral to membrane (GO:0042613; GO:0016021) [B2XBN8] [c]	3.192	0.232
CA052037	MTERF domain containing 1 [AAH12995; *Homo sapiens*] [(X)]	185 (66%)	2E-69	Promoter binding (GO:0010843) [Q96E29]	2.369	0.274
EG808887	Myosin heavy chain [BAG16351; *Coryphaenoides yaquinae*]	129 (91%)	1E-68	ATP binding; Actin binding; Motor activity (GO:0005524; GO:0003779; GO:0003774) [B1Q382]	2.709	0.742
FC072731	Neuromedin s [ACJ64069; *Danio rerio*]	98 (51%)	4E-17	Unknown	2.354	0.268
EG868345	QIL1 [AAM14633; *Mus musculus*] [(X)]	119 (35%)	5E-13	Mitochondrion (GO:0005739) [Q8R404] [c]	1.968	0.256
EG765364	Ras-related protein Rab-27A [ACO09389; *Osmerus mordax*]/[EZ770488; *Oncorhynchus mykiss*] [(B)]	185 (92%)/ 166 (92%)	2E-104/ 3E-54	GTP binding (GO:0005525) [C1BK36]	2.532	0.567
EG924794	Retinoic acid receptor gamma b (Rargb) gene [EU025716; *Salmo salar*] [(N)]	328 (84%)	2E-76	Sequence-specific DNA binding; Transcription factor activity (GO:0043565; GO:0003700) [B3SU91]	2.050	0.161
CA037366	Rhamnose binding lectin STL1 [BAA92255; *Oncorhynchus mykiss*]	55 (87%)	4E-23	Sugar binding (GO:0005529) [Q9IB53]	2.318	0.433

CA064204	S100 calcium binding protein, beta (neural) [BT056444; *Salmo salar*] (N)	391 (100%)	0	Calcium ion binding (GO:0005509) [Q6DGT8]	19.943	15.974
CA061332	Splicing factor, arginine/serine-rich 7 [BT056940; *Salmo salar*] (N)	550 (99%)	0	Nucleic acid binding; Nucleotide binding; Zinc ion binding (GO:0003676; GO:0000166; GO:0008270) [B9EMR5]	1.883	0.256
DY734333	Tripartite motif-containing protein 16 [ACI34059; *Salmo salar*]	74 (76%)	4E-26	Zinc ion binding (GO:0008270) [B5X428]	3.512	0.552
EG913553	Tripartite motif-containing protein 16 [ACI34059; *Salmo salar*]	152 (76%)	3E-62	Zinc ion binding (GO:0008270) [B5X428]	3.457	0.958
CX033589	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.424	0.271
DW562515	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.629	0.926
DW543362	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.469	0.996
CA058359	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.350	1.246

Please see Appendix II for footnotes.

APPENDIX IV. Supplemental table containing 442 transcripts with greater than 2-fold higher expression in triploid growth hormone transgenic (3NGHTg) Atlantic salmon family AS26 (fast-growing) in comparison to 3NGHTg Atlantic salmon family AS25 (slow-growing) in any 3 out of 4 technical replicate microarrays including at least one dye-swap.

EST	Gene Name of Best BLASTX or BLASTN (N) Hit	Length (% ID)	E value	Function of Best BLAST Hit	$\overline{X}$ Fold Change	SE
CB496601	15-hydroxyprostaglandin dehydrogenase [ACI69905; *Salmo salar*]	139 (95%)	6E-65	Binding; Oxidoreductase activity (GO:0005488; GO:0016491) [B5XGD5]	3.054	0.209
CB492983	2-peptidylprolyl isomerase A [ACH70768; *Salmo salar*] (*Oncorhynchus mykiss* feature)	93 (100%)	5E-55	Peptidyl-prolyl cis-trans isomerase activity (GO:0003755) [B5DG99]	2.149	0.228
CB493346	2-peptidylprolyl isomerase A [ACH70768; *Salmo salar*] (*Oncorhynchus mykiss* feature)	95 (82%)	1E-39	Peptidyl-prolyl cis-trans isomerase activity (GO:0003755) [B5DG99]	2.796	0.386
CA045317	3-ketoacyl-CoA thiolase [BT045547; *Salmo salar*] (N)	686 (99%)	0	Ransferase activity, transferring acyl groups other than amino-acyl groups (GO:0016747) [B5X3C8]	2.556	0.259
CB511716	35 kDa SR repressor protein [BT059492; *Salmo salar*] (N)	855 (99%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [C0HAY6]	4.057	1.402
CA042535	40 kDa peptidyl-prolyl cis-trans isomerase [ACO07506; *Oncorhynchus mykiss*]	103 (100%)	7E-47	Binding; Peptidyl-prolyl cis-trans isomerase activity (GO:0005488; GO:0003755) [C1BEQ3]	11.138	3.077
CB492405	40S ribosomal protein S11 [ACO15454; *Caligus clemensi*]	105 (100%)	3E-54	Structural constituent of ribosome (GO:0003735) [C1C2F1]	10.159	0.693
CB510129	40S ribosomal protein S12 [ACH70842; *Salmo salar*]	132 (100%)	6E-70	Structural constituent of ribosome (GO:0003735) [B5DGG8]	2.483	0.339

CB491393	40S ribosomal protein S13 [ACO08029; *Oncorhynchus mykiss*]	139 (99%)	9E-73	Structural constituent of ribosome (GO:0003735) [C1BG76]	71.861	34.008
CB494485	40S ribosomal protein S14 [ACN09966; *Salmo salar*]	143 (100%)	1E-75	Structural constituent of ribosome (GO:0003735) [C0H7E7]	2.280	0.463
CK990659	40S ribosomal protein S15 [ACN10008; *Salmo salar*]	147 (96%)	5E-50	RNA binding; Structural constituent of ribosome (GO:0003723; GO:0003735) [C0H7I9]	5.128	1.507
CA041970	40s ribosomal protein S16 [ACH70747; *Salmo salar*] (*Salmo salar* feature)	146 (100%)	8E-77	Structural constituent of ribosome (GO:0003735) [B5DG73]	3.578	0.559
CB492970	40S ribosomal protein S16 [ACN10073; *Salmo salar*] (*Oncorhynchus mykiss* feature)	146 (100%)	4E-77	Structural constituent of ribosome (GO:0003735) [C0H7Q4]	3.114	0.697
CB510968	40S ribosomal protein S16 [ACN10073; *Salmo salar*] (*Salmo salar* feature)	146 (100%)	9E-77	Structural constituent of ribosome (GO:0003735) [C0H7Q4]	3.648	0.348
CB508535	40S ribosomal protein S23 [ACN10021; *Salmo salar*]	145 (100%)	2E-78	Structural constituent of ribosome (GO:0003735) [C0H7K2]	2.955	0.743
CB494375	40S ribosomal protein S24 [BT044043; *Salmo salar*] (N)	118 (98%)	7E-48	Nucleotide binding; Structural constituent of ribosome (GO:0000166; GO:0003735) [B5RIB9]	2.657	0.220
CB492902	40S ribosomal protein S27 [ABJ98653; *Psetta maxima*] (*Oncorhynchus mykiss* feature)	87 (98%)	1E-44	Structural constituent of ribosome (GO:0003735) [A0EZY9]	5.923	1.641
CB492978	40S ribosomal protein S27 [ABJ98653; *Psetta maxima*] (*Oncorhynchus mykiss* feature)	87 (98%)	1E-37	Structural constituent of ribosome (GO:0003735) [A0EZY9]	4.091	0.914
CB497260	40S ribosomal protein S4 [ACN10029; *Salmo salar*] (*Oncorhynchus mykiss* feature)	178 (100%)	6E-98	Structural constituent of ribosome (GO:0003735) [C0H7L0]	2.333	0.171

CB497635	40S ribosomal protein S4 [ACN12376; *Salmo salar*] (*Oncorhynchus mykiss* feature)	177 (99%)	1E-95	Structural constituent of ribosome (GO:0003735) [C0H7L0]	33.052	24.103
CB496987	40S ribosomal protein S6 [ACN09990; *Salmo salar*]	185 (100%)	2E-100	Structural constituent of ribosome (GO:0003735) [C0H7H1]	2.472	0.284
CA042530	6-phosphofructokinase, liver type [AAI26579; *Bos taurus*]	199 (78%)	9E-87	6-phosphofructokinase activity; ATP binding; Metal ion binding (GO:0003872; GO:0005524; GO:0046872) [A1A4J1]	2.544	0.545
CB510252	60S ribosomal protein L10 [ACN10030; *Salmo salar*]	210 (100%)	4E-121	Structural constituent of ribosome (GO:0003735) [C0H7L1]	3.190	0.860
CB494510	60S ribosomal protein L11 [ACI69075; *Salmo salar*] (*Oncorhynchus mykiss* feature)	177 (100%)	1E-97	Structural constituent of ribosome (GO:0003735) [B5XE05]	6.707	1.835
CB511063	60S ribosomal protein L11 [ACI69075; *Salmo salar*] (*Salmo salar* feature)	171 (99%)	6E-94	Structural constituent of ribosome (GO:0003735) [B5XE05]	2.729	0.191
CA037667	60S ribosomal protein L13a [ACN10380; *Salmo salar*]	192 (100%)	4E-94	Structural constituent of ribosome (GO:0003735) [C0H8L1]	2.279	0.476
CB498637	60S ribosomal protein L19 [ACN09972; *Salmo salar*]	162 (99%)	2E-52	Structural constituent of ribosome (GO:0003735) [C0H7F3]	3.760	1.144
CA044118	60S ribosomal protein L21 [ACH70979; *Salmo salar*]	160 (100%)	3E-88	Structural constituent of ribosome (GO:0003735) [B5DGV5]	2.202	0.196
CB509769	60S ribosomal protein L27a [ACI66567; *Salmo salar*]	147 (100%)	2E-70	Structural constituent of ribosome (GO:0003735) [B5X6U7]	2.476	0.154
CA042354	60S ribosomal protein L28 [ACO07782; *Oncorhynchus mykiss*]	105 (99%)	1E-64	Structural constituent of ribosome (GO:0003735) [C1BFH9]	2.995	0.700
BU965787	60S ribosomal protein L29 [ACO13335; *Esox lucius*]	54 (100%)	9E-25	Structural constituent of ribosome (GO:0003735) [C1BWD2]	4.519	0.981
CB496918	60S ribosomal protein L3	205 (99%)	8E-115	Structural constituent of ribosome	2.697	0.182

	[ACI66814; *Salmo salar*] (*Oncorhynchus mykiss* feature)			(GO:0003735) [B5X7J4]		
CA042790	60S ribosomal protein L3 [ACI68315; *Salmo salar*] (*Salmo salar* feature)	123 (99%)	3E-68	Structural constituent of ribosome (GO:0003735) [B5XBU5]	12.451	8.191
CB493650	60S ribosomal protein L31 [ACN09978; *Salmo salar*]	130 (97%)	6E-57	Structural constituent of ribosome (GO:0003735) [C0H7F9]	2.494	0.302
CA047190	60S ribosomal protein L35 [ACI66532; *Salmo salar*] (*Salmo salar* feature)	123 (100%)	2E-49	Structural constituent of ribosome (GO:0003735) [B5X6R2]	5.350	2.256
CB487751	60S ribosomal protein L35 [ACI67490; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	123 (99%)	1E-46	Structural constituent of ribosome (GO:0003735) [B5X9H0]	3.041	0.880
CB498295	60S ribosomal protein L35 [BT047689; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* type 2)	407 (94%)	8E-167	Structural constituent of ribosome (GO:0003735) [B5X9H0]	2.713	0.639
CB494678	60S ribosomal protein L35a [ACN09951; *Salmo salar*]	110 (100%)	3E-58	Structural constituent of ribosome (GO:0003735) [C0H7D2]	2.788	0.298
CB501730	60S ribosomal protein L36 [ACI67440; *Salmo salar*] (*Salmo salar* type 1)	60 (99%)	5E-30	Structural constituent of ribosome (GO:0003735) [B5X9C0]	2.406	0.197
CA037622	60S ribosomal protein L36 [ACI68713; *Salmo salar*] (*Salmo salar* type 2)	108 (99%)	3E-47	Structural constituent of ribosome (GO:0003735) [B5XCZ3]	2.376	0.615
CB494242	60S ribosomal protein L36 [ACI68713; *Salmo salar*] (*Oncorhynchus mykiss* feature)	100 (97%)	3E-48	Structural constituent of ribosome (GO:0003735) [B5XCZ3]	2.100	0.308
CB497661	60S ribosomal protein L36 [ACI68713; *Salmo salar*] (*Oncorhynchus mykiss* feature)	99 (97%)	2E-47	Structural constituent of ribosome (GO:0003735) [B5XCZ3]	2.759	0.549
CB507058	60S ribosomal protein L36a-1	106 (96%)	4E-45	Structural constituent of ribosome	4.091	1.208

	[ACH70983; *Salmo salar*] (*Salmo salar* type 3)			(GO:0003735) [B5DGV9]		
FC072883	60S ribosomal protein L37 [ACN09993; *Salmo salar*]	93 (89%)	6E-40	Structural constituent of ribosome (GO:0003735) [C0H7H4]	3.736	0.817
CB487825	60S ribosomal protein L38 [ACN10033; *Salmo salar*]	48 (94%)	4E-17	Structural constituent of ribosome (GO:0003735) [C0H7L4]	3.145	0.850
CB497459	60S ribosomal protein L5 [ACO07720; *Oncorhynchus mykiss*]	213 (100%)	7E-109	5S rRNA binding; Structural constituent of ribosome (GO:0008097; GO:0003735) [C1BFB7]	4.768	1.219
CB492750	60S ribosomal protein L7 [ACO07661; *Oncorhynchus mykiss*]	157 (76%)	5E-56	Structural constituent of ribosome; Transcription regulator activity (GO:0003735; GO:0030528) [C1BF58]	2.947	0.264
CB511183	60S ribosomal protein L7a [ACN10320; *Salmo salar*]	164 (100%)	1E-78	Ribosome (GO:0005840) [C0H8F1] [c]	3.483	0.407
CB494677	60S ribosomal protein L8-1 [ACH70990; *Salmo salar*]	205 (86%)	5E-88	Structural constituent of ribosome (GO:0003735) [B5DGW6]	3.822	1.697
CB492853	60S ribosomal protein L9 [ACH70676; *Salmo salar*] (*Oncorhynchus mykiss* feature)	139 (100%)	3E-72	rRNA binding; Structural constituent of ribosome (GO:0019843; GO:0003735) [B5DG02]	3.066	0.372
CB496532	60S ribosomal protein L9 [ACH70676; *Salmo salar*] (*Oncorhynchus mykiss* feature)	123 (100%)	5E-62	rRNA binding; Structural constituent of ribosome (GO:0019843; GO:0003735) [B5DG02]	2.264	0.198
CK991300	60S ribosomal protein L9 [ACH70676; *Salmo salar*] (*Oncorhynchus mykiss* feature)	116 (95%)	3E-52	rRNA binding; Structural constituent of ribosome (GO:0019843; GO:0003735) [B5DG02]	1.904	0.246
CB510651	72 kDa type IV collagenase precursor [BT072163; *Salmo salar*] [(N)]	688 (100%)	0	Metalloendopeptidase activity; Zinc ion binding (GO:0004222; GO:0008270) [C0PU91]	34.233	16.896
EG779795	Actin related protein 2/3 complex 16 kD subunit, putative [EEB11863; *Pediculus humanus*	149 (37%)	5E-15	Cytoskeleton (GO:0005856) [E0VEQ7] [c]	3.659	1.628

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CB509930	Actin-related protein 2/3 complex subunit 4 [BT060120; *Salmo salar*] (N)	429 (99%)	0	Cytoskeleton (GO:0005856) [C0H7W0] [c]	5.570	2.051
CB493998	Actin-related protein 2/3 complex subunit 5 [BT125478; *Salmo salar*] (N)	681 (89%)	0	Cytoskeleton (GO:0005856) [B5XCZ5] [c]	2.654	0.631
CA043188	Acyl carrier protein, mitochondrial precursor [BT048253; *Salmo salar*] (N)	292 (91%)	4E-97	Acyl carrier activity; Cofactor binding; Phosphopantetheine binding (GO:0000036; GO:0048037; GO:0031177) [B5XB34]	3.460	0.482
CB510709	Acyl-CoA synthetase [BT059131; *Salmo salar*] (N)	214 (91%)	1E-70	Catalytic activity (GO:0003824) [B5X460]	2.097	0.199
CB493696	Acyl-CoA-binding protein [ACI68322; *Salmo salar*] (ACBP, Fig. 11A)	42 (95%)	9E-16	Fatty-acyl-CoA binding (GO:0000062) [B5XBV2]	6.177	1.684
CB493265	Adenine nucleotide translocator s598 [BAD86711; *Takifugu rubripes*]	41 (88%)	1E-23	Binding; Transporter activity (GO:0005488; GO:0005215) [Q5KSP2]	2.246	0.394
CA058864	ADP-ribosylation factor 1 [ACI33932; *Salmo salar*]	63 (99%)	7E-28	GTP binding (GO:0005525) [B5X3Q1]	2.516	0.525
CA050777	ADP-ribosylation factor-like protein 8B [BT046252; *Salmo salar*] (N)	716 (99%)	0	GTP binding (GO:0005525) [B5X5D3]	4.762	2.651
CK990577	ADP/ATP translocase 2 [ACI67091; *Salmo salar*]	38 (95%)	2E-12	Binding; Transporter activity (GO:0005488; GO:0005215) [B5X8C1]	62.375	59.964
CB496841	AE binding protein 1 [CAX12167; *Danio rerio*]/[EZ819625; *Oncorhynchus nerka*] (B)	166 (78%)/ 182 (99%)	2E-74/ 2E-87	Metallocarboxypeptidase activity; Zinc ion binding (GO:0004181; GO:0008270) [B8JM73]	4.632	1.118
CX035072	Alpha-2-macroglobulin-2	164 (75%)	1E-87	Endopeptidase inhibitor activity	11.442	3.454

	[BAA85039; *Cyprinus carpio*]			(GO:0004866) [Q9PVU4]		
CA043158	Alpha-aspartyl dipeptidase [ACI68014; *Salmo salar*]	111 (100%)	3E-58	Serine-type peptidase activity (GO:0008236) [B5XAZ4]	2.401	0.231
CB492263	Alpha-globin I [BAA13533; *Oncorhynchus mykiss*]	143 (100%)	1E-76	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [Q98973]	3.514	0.264
CB510583	Aminopeptidase [CAA72813; *Lumbricus rubellus*]	125 (65%)	1E-43	Aminopeptidase activity (GO:0004177) [O01357]	5.853	1.324
CB510708	Angiotensinogen precursor [BT045876; *Salmo salar*] [(N)]	101 (90%)	2E-24	Serine-type endopeptidase inhibitor activity (GO:0004867) [B5X4A7]	6.264	3.123
CA038790	Antithrombin [CAB64714; *Salmo salar*]	145 (98%)	4E-106	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q9PTA8]	4.382	0.831
CA041892	Apolipoprotein A-I precursor [ACI68193; *Salmo salar*] (*Salmo salar* type 2) (APOAI-2, Fig. 12B)	44 (100%)	3E-16	Lipid binding (GO:0008289) [B5XBH3]	92.395	54.150
CB506105	Apolipoprotein A-I precursor [ACI68193; *Salmo salar*] (*Salmo salar* type 2) (APOAI-2, Fig. 12B)	143 (100%)	3E-62	Lipid binding (GO:0008289) [B5XBH3]	3.106	0.384
CB494614	Apolipoprotein A-I-1 [AAB96972; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* type 1) (APOAI-1, Fig. 12A)	120 (99%)	7E-48	Lipid binding (GO:0008289) [O57523]	2.900	0.506
CB498079	Apolipoprotein A-II [BAH58380; *Oncorhynchus mykiss*]	143 (100%)	1E-63	Unknown	3.019	0.825
CB493958	Apolipoprotein A-IV precursor [ACI67266; *Salmo salar*] (APOAIV, Fig. 11B)	121 (98%)	3E-57	Lipid binding (GO:0008289) [B5X8U6]	4.561	0.959
CA047039	Apolipoprotein C-I precursor [ACI69086; *Salmo salar*] (*Salmo*	65 (100%)	2E-32	Extracellular region (GO:0005576) [B5XE16] [c]	3.200	0.511

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CB491411	Apolipoprotein C-I precursor [ACI69086; *Salmo salar*] (*Oncorhynchus mykiss* feature)	87 (96%)	4E-39	Extracellular region (GO:0005576) [B5XE16] [c]	8.738	1.988
EG767982	Aspartyl/asparaginyl beta-hydroxylase [ACO14201; *Esox lucius*]/[EZ771405; *Oncorhynchus mykiss*] [(B)]	185 (64%)/ 397 (91%)	4E-44/ 3E-138	Membrane (GO:0016020) [C1BYU8] [c]	10.816	7.095
CB497584	ATP synthase H+ transporting mitochondrial F1 complex beta [ACH85277; *Salmo salar*]	115 (100%)	7E-57	ATP binding; Hydrogen ion transporting ATP synthase activity, rotational mechanism; Hydrogen-exporting ATPase activity, phosphorylative mechanism; Proton-transporting ATPase activity, rotational mechanism (GO:0005524; GO:0046933; GO:0008553; GO:0046961) [B5RI36]	4.536	1.616
CB493213	ATP synthase lipid-binding protein, mitochondrial precursor [ACN09821; *Salmo salar*]	137 (98%)	6E-54	Hydrogen ion transporting ATP synthase activity, rotational mechanism (GO:0046933) [C0H702]	2.355	0.434
CB492831	ATP synthase subunit O, mitochondrial precursor [ACI68940; *Salmo salar*]	187 (100%)	2E-90	Hydrogen ion transporting ATP synthase activity, rotational mechanism (GO:0046933) [B5XDM0]	10.598	7.507
BU965693	ATP synthase-coupling factor 6, mitochondrial precursor [ACI66451; *Salmo salar*]	108 (100%)	8E-53	Hydrogen ion transmembrane transporter activity (GO:0015078) [B5X6I1]	2.158	0.358
CA057485	ATP-binding cassette sub-family F member 1 [BT072466; *Salmo salar*] [(N)]	674 (99%)	0	Unknown	3.490	0.967
CB496943	ATP-dependent RNA helicase DDX39 [ACN58701; *Salmo salar*]	148 (99%)	2E-76	ATP binding; ATP-dependent helicase activity; Nucleic acid binding (GO:0005524; GO:0008026; GO:0003676) [C0PUM3]	9.931	5.430

CA038250	Autophagy-related protein 13 [DAA21766; *Bos taurus*]	132 (66%)	7E-34	Unknown	2.553	0.373
DY710489	B lymphocyte induced maturation protein 1 [BAD02932; *Takifugu rubripes*]	152 (72%)	5E-51	Nucleic acid binding; Zinc ion binding (GO:0003676; GO:0008270) [Q75UA3]	2.827	0.753
CA043347	B-cell translocation gene 1 [ACI33931; *Salmo salar*]	163 (100%)	2E-86	Unknown	4.609	0.615
CA057098	Barrier-to-autointegration factor [ACI68033; *Salmo salar*]	97 (100%)	4E-52	DNA binding (GO:0003677) [B5RI51]	2.212	0.136
CA056920	Barrier-to-autointegration factor B [BT048804; *Salmo salar*] [(N)]	100 (92%)	8E-29	DNA binding (GO:0003677) [B5XCN5]	3.630	1.578
CB494537	Basic transcription factor 3-1 [ACH70908; *Salmo salar*]	149 (100%)	5E-65	Unknown	13.437	8.243
EG901382	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 [ACI66775; *Salmo salar*]	187 (100%)	4E-96	Integral to membrane; Mitochondrial envelope (GO:0016021; GO:0005740) [B5X7F5] [c]	3.509	0.442
CB498391	Beta-2 microglobulin [AAB04653; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	116 (100%)	4E-62	MHC class I protein complex (GO:0042612) [Q91966] [c]	4.216	0.952
CB500803	Beta-2 microglobulin [AF180486; *Salmo salar*] [(N)] (*Salmo salar* type 1) (B2M1, Fig. 14A)	661 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DG62] [c]	2.315	0.377
CB505594	Beta-2 microglobulin [AF180486; *Salmo salar*] [(N)] (*Salmo salar* type 1) (B2M1, Fig. 14A)	799 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DG62] [c]	3.594	0.417
CB509521	Beta-2-glycoprotein 1 precursor [ACN10110; *Salmo salar*] (*Salmo salar* type 1)	211 (84%)	3E-110	Unknown	5.587	0.632
CA038031	Beta-2-glycoprotein 1 precursor [ACN10110; *Salmo salar*]	132 (96%)	1E-71	Unknown	2.599	0.309

	(*Salmo salar* type 2)					
CB500982	Beta-2-microglobulin precursor [BT046451; *Salmo salar*] [(N)] (*Salmo salar* type 1) (B2M1, Fig. 14A)	752 (100%)	0	MHC class I protein complex (GO:0042612) [B5X5Y2] [c]	2.652	0.287
CA043324	Beta-2-microglobulin precursor [BT047559; *Salmo salar*] [(N)] (*Salmo salar* type 2) (B2M2, Fig. 14B)	542 (99%)	0	MHC class I protein complex (GO:0042612) [Q9DD81] [c]	27.441	12.848
CB509758	Beta-globin [CAA65945; *Salmo salar*]	148 (100%)	2E-79	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [Q91473]	2.789	0.538
CB509986	Beta-ureidopropionase [ACM08325; *Salmo salar*]	81 (100%)	8E-40	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds (GO:0016810) [B9ELC8]	4.465	2.108
CB510234	Bile salt export pump [ABJ55520; *Oncorhynchus mykiss*]	99 (99%)	1E-40	ATP binding; ATPase activity, coupled to transmembrane movement of substances (GO:0005524; GO:0042626) [A0MH69]	4.176	0.709
CB492660	Biotinidase fragment 1 [AAG30007; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	111 (99%)	7E-57	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides (GO:0016811) [Q9DFF8]	2.944	0.554
CB497307	Biotinidase fragment 1 [AAG30007; Oncorhynchus mykiss] (*Oncorhynchus mykiss* feature)	114 (97%)	5E-57	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides (GO:0016811) [Q9DFF8]	2.802	0.300
CB510905	Brain protein 44-like protein [ACI66404; *Salmo salar*] (*Salmo salar* type 1)	80 (100%)	2E-39	Unknown	2.624	0.077
CB509993	Brain protein 44-like protein [ACI66612; *Salmo salar*] (*Salmo salar* type 2)	60 (100%)	1E-26	Unknown	3.645	0.378

CK991275	Brain protein 44-like protein [ACO07659; *Oncorhynchus mykiss*] (*Salmo salar* type 3)	71 (96%)	3E-31	Unknown	20.324	13.186
CA062798	Bridging integrator 2 [BT058800; *Salmo salar*] [(N)]	83 (97%)	2E-28	Cytoplasm (GO:0005737) [C0H8Z4] [c]	2.833	0.433
CA369135	C type lectin receptor C [AAT77222; *Salmo salar*]	186 (94%)	1E-76	Receptor activity; Sugar binding (GO:0004872; GO:0005529) [Q68S96]	6.150	2.455
CA768280	C-4 methylsterol oxidase [ACO09899; *Osmerus mordax*]/[EZ782524; *Oncorhynchus mykiss*] [(B)]	92 (91%)/ 265 (94%)	2E-46/ 2E-104	Iron ion binding; Oxidoreductase activity (GO:0005506; GO:0016491) [C1BLJ6]	2.903	0.415
CB511048	C-type lectin domain family 4 member E [ACI67923; *Salmo salar*]	27 (100%)	1E-8	Sugar binding (GO:0005529) [B5XAQ3]	8.295	3.675
CB492852	C-type MBL-2 protein [CAJ14130; *Oncorhynchus mykiss*]	145 (100%)	1E-97	Sugar binding (GO:0005529) [Q4LAN6]	3.423	0.782
CB508151	C1q and tumor necrosis factor-like protein 2 protein [ACJ60645; *Sus scrofa*]/[EZ887220; *Oncorhynchus mykiss*] [(B)]	37 (90%)/ 261 (95%)	1E-11/ 4e-106	Unknown	2.725	0.406
CA055233	Calreticulin precursor [BT072764; *Salmo salar*] [(N)]	684 (99%)	0	Calcium ion binding; Unfolded protein binding (GO:0005509; GO:0051082) [C0PUU5]	2.408	0.285
CA346186	CD151 antigen [AAH65859; *Danio rerio*]	128 (88%)	1E-54	Integral to membrane (GO:0016021) [Q6P031] [c]	2.954	0.443
CA053693	CD166 antigen homolog precursor [BT072099; *Salmo salar*] [(N)]	778 (100%)	0	Unknown	2.363	0.318
CA037551	Coagulation factor IX precursor [AAO33372|AF465277;	73 (81%)	2E-31	Calcium ion binding; Serine-type endopeptidase activity (GO:0005509;	13.747	8.029

	Takifugu rubripes] (*Salmo salar* type 2)			GO:0004252) [Q804W8]		
CB509382	Coagulation factor IX precursor [BT059341; *Salmo salar*] [(N)] (*Salmo salar* type 1)	707 (100%)	0	Calcium ion binding; Serine-type endopeptidase activity (GO:0005509; GO:0004252) [C0HAI5]	5.150	1.836
CB494727	Cold-inducible RNA-binding protein [BT057316; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* type 2)	481 (96%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [B5DGC5]	15.481	5.728
CA044962	Cold-inducible RNA-binding protein [BT058753; *Salmo salar*] [(N)] (*Salmo salar* feature)	514 (99%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [C0H8U7]	14.522	10.420
CB492859	Cold-inducible RNA-binding protein [BT125559; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* type 1)	594 (96%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [E0R8Z1]	2.860	0.371
CB496934	Cold-inducible RNA-binding protein [BT125559; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* type 1)	605 (95%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [E0R8Z1]	4.255	0.905
CB511435	Complement factor Bf-1 [AAC83699; *Oncorhynchus mykiss gairdneri*]	151 (76%)	3E-62	Serine-type endopeptidase activity (GO:0004252) [Q9YGE7]	4.470	0.849
CB509933	Complement factor H precursor [CAF25505; *Oncorhynchus mykiss*] (*Salmo salar* feature)	137 (76%)	1E-55	Unknown	5.724	1.991
CB493785	Complement factor H1 protein [ABY55261; *Oncorhynchus masou formosanus*] (*Oncorhynchus mykiss* feature)	149 (82%)	2E-69	Unknown	17.582	10.610
CB497097	Complement factor H1 protein [ABY55261; *Oncorhynchus*	117 (86%)	2E-56	Unknown	3.193	0.745

	masou formosanus] (*Oncorhynchus mykiss* feature)					
CX260651	Cyclic AMP-dependent transcription factor ATF-5 [BT059632; *Salmo salar*] [(N)]	526 (95%)	0	Protein dimerization activity; Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity (GO:0046983; GO:0043565; GO:0003700) [C0HBC6]	2.439	0.766
CK990833	Cystatin-B [ACI69028; *Salmo salar*]	98 (93%)	6E-46	Cysteine-type endopeptidase inhibitor activity (GO:0004869) [B5XDV8]	2.488	0.450
EG798235	Cytochrome b-c1 complex subunit 7 [ACI66572; *Salmo salar*]	110 (100%)	1E-48	Ubiquinol-cytochrome-c reductase activity (GO:0008121) [B5X6V2]	5.719	1.964
CB496806	Cytochrome c oxidase polypeptide VIa, mitochondrial precursor [ACI66605; *Salmo salar*] (*Oncorhynchus mykiss* feature)	102 (99%)	8E-47	Cytochrome-c oxidase activity (GO:0004129) [B5X6Y5]	2.768	0.293
CA042792	Cytochrome c oxidase polypeptide VIa, mitochondrial precursor [ACI69150; *Salmo salar*] (*Salmo salar* feature)	102 (100%)	4E-47	Cytochrome-c oxidase activity (GO:0004129) [B5XE80]	2.314	0.257
CB496455	Cytochrome c oxidase polypeptide VIIb, mitochondrial precursor [ACI67848; *Salmo salar*]	79 (99%)	2E-39	Cytochrome-c oxidase activity (GO:0004129) [B5XAH8]	4.866	2.471
CB510326	Cytochrome c oxidase subunit 4 isoform 2, mitochondrial precursor [ACI67065; *Salmo salar*]	177 (100%)	4E-97	Cytochrome-c oxidase activity (GO:0004129) [B5X895]	2.646	0.464
CB492792	Cytochrome c oxidase subunit 5B, mitochondrial precursor [ACO07893; *Oncorhynchus mykiss*]	117 (99%)	2E-64	Cytochrome-c oxidase activity (GO:0004129) [C1BFU0]	2.249	0.355

CB512292	Cytochrome c oxidase subunit VIb isoform 1 [ACI67996; *Salmo salar*]	86 (100%)	9E-47	Cytochrome-c oxidase activity (GO:0004129) [B5XAX6]	2.152	0.284
CN442513	Cytochrome oxidase subunit II [AAD04736; *Salmo salar*]	226 (94%)	6E-102	Unknown	9.931	4.204
CA042231	Cytochrome P450 [AAG30296; *Ictalurus punctatus*]	204 (76%)	1E-90	Electron carrier activity; Heme binding; Monooxygenase activity (GO:0009055; GO:0020037; GO:0004497) [Q9DEW9]	2.018	0.152
EG832531	Cytochrome P450 monooxygenase [AAC26494; *Oncorhynchus mykiss*]	218 (94%)	6E-116	Aromatase activity; Electron carrier activity; Heme binding (GO:0070330; GO:0009055; GO:0020037) [O93299]	3.452	0.700
EG901171	Cytochrome P450, family 2, subfamily J, polypeptide 24 [AAI54482; *Danio rerio*]	133 (76%)	2E-56	Electron carrier activity; Heme binding; Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen (GO:0009055; GO:0020037; GO:0016712) [Q5TZ75]	2.498	0.519
CA053929	Cytoplasmic tRNA 2-thiolation protein 2 [DAA20129; *Bos taurus*]/[BT072492; *Salmo salar*] [(B)]	327 (57%)/ 507 (99%)	1E-90/ 0	Unknown	3.664	0.826
CA037683	Delta-6 fatty acyl desaturase D6fad_a [AAR21624; *Salmo salar*]	51 (100%)	3E-22	Heme binding; Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [Q6SES0]	2.278	0.200
CB493595	Delta5-desaturase-like protein [ABU87822; *Oncorhynchus masou*] (D5DP, Fig. 11C)	87 (99%)	2E-45	Heme binding; Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037;	3.245	0.359

				GO:0016717) [A7XUS7]		
CA043090	Diacylglycerol O-acyltransferase 2 [AAH96927; *Danio rerio*] (*Salmo salar* type 1)	31 (94%)	4E-10	Diacylglycerol O-acyltransferase activity (GO:0004144) [Q4V9F0]	9.509	6.215
EG864429	Diacylglycerol O-acyltransferase 2 like 1 a protein [AAH45058; *Xenopus laevis*] (*Salmo salar* type 2)	107 (65%)	1E-36	2-Acylglycerol O-acyltransferase activity (GO:0003846) [Q3KPP4]	4.157	1.553
CB511033	Diamine acetyltransferase 1 [ACI67505; *Salmo salar*]	113 (100%)	5E-59	N-acetyltransferase activity (GO:0008080) [B5X9I5]	18.235	11.020
CA046376	Differentially regulated trout protein 1 [AAG30030|AF281355; *Oncorhynchus mykiss*] (*Salmo salar* feature)	88 (96%)	4E-44	Unknown	3.760	1.045
CK990321	Differentially regulated trout protein 1 [AAG30030|AF281355; *Oncorhynchus mykiss*] (*Salmo salar* feature)	55 (91%)	6E-35	Unknown	2.781	0.551
CA043782	DNA polymerase subunit delta-4 [ACM09657; *Salmo salar*]	112 (100%)	1E-52	Nucleus (GO:0005634) [B9EQ60] [c]	11.614	8.518
CB496981	DNA-directed RNA polymerases I, II, and III subunit RPABC2 [ACO13758; *Esox lucius*] (*Oncorhynchus mykiss* feature)	56 (98%)	4E-24	DNA binding; DNA-directed RNA polymerase activity (GO:0003677; GO:0003899) [C1BXK5]	4.332	1.070
CK991257	DNA-directed RNA polymerases I, II, and III subunit RPABC2 [BT056477; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* feature)	485 (91%)	1E-173	DNA binding; DNA-directed RNA polymerase activity (GO:0003677; GO:0003899) [B9ELF2]	4.528	1.327
CA044549	DnaJ homolog subfamily A member 2 [BT057967; *Salmo*	437 (99%)	0	Heat shock protein binding; Unfolded protein binding (GO:0031072;	2.548	0.417

	salar] (N)			GO:0051082) [B9EQP2]		
CB510989	Dual specificity protein kinase CLK4 [BT045149; *Salmo salar*] (N)	260 (78%)	5E-25	ATP binding; Protein serine/threonine kinase activity (GO:0005524; GO:0004674) [B5X280]	2.212	0.360
CB498428	Early meiotic induction protein 5, mitochondrial precursor [ACO08273; *Oncorhynchus mykiss*]	163 (94%)	1E-83	Unknown	5.802	3.436
CA042698	Elongation factor 1-alpha [ACN10642; *Salmo salar*] (*Salmo salar* feature)	99 (100%)	2E-49	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	6.019	1.174
CB497678	Elongation factor 1-alpha [ACN10642; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	51 (100%)	2E-20	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	3.350	0.321
CB498324	Elongation factor 1-alpha [ACN10642; *Salmo salar*] (*Oncorhynchus mykiss* type 2)	145 (100%)	2E-77	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	36.190	21.524
CA060826	Elongation factor 1-alpha 1 [ACN11490; *Salmo salar*] (*Salmo salar* feature)	38 (100%)	1E-11	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	57.398	37.077
CA055797	Elongation factor 1-gamma [ACI33692; *Salmo salar*] (*Salmo salar* feature)	122 (100%)	6E-69	Translation elongation factor activity (GO:0003746) [B5X311]	2.767	0.573
CB493290	Elongation factor 1-gamma [ACN10123; *Salmo salar*] (*Oncorhynchus mykiss* feature)	73 (92%)	2E-53	Translation elongation factor activity (GO:0003746) [C0H7V4]	2.691	0.298
CB498321	Elongation factor 2 [ACN10751; *Salmo salar*]	211 (99%)	3E-104	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9N2]	44.294	28.274
EG884003	Endoplasmic reticulum-Golgi intermediate compartment protein 3 [AAI00126; *Danio*	32 (91%)	9E-12	ER-Golgi intermediate compartment membrane; Golgi apparatus; Endoplasmic reticulum membrane;	6.044	1.857

	rerio] [X]			Integral to membrane (GO:0033116; GO:0005794; GO:0005789; GO:0016021) [Q803I2] [c]		
CB494346	Enolase 3-1 [ACH70930; *Salmo salar*]	182 (99%)	3E-101	Magnesium ion binding; Phosphopyruvate hydratase activity (GO:0000287; GO:0004634) [B5DGQ6]	6.288	1.649
CA057166	Enolase 3-2 [ACH70931; *Salmo salar*]	167 (99%)	1E-91	Magnesium ion binding; Phosphopyruvate hydratase activity (GO:0000287; GO:0004634) [B5DGQ7]	2.105	0.121
CA064237	Erythrocyte membrane protein band 4.1-like 3 [EAX01645; *Homo sapiens*]/[EZ784403; *Oncorhynchus mykiss*] [B]	96 (89%)/ 728 (95%)	9E-26/ 0	Unknown	12.742	4.792
CB512374	Ester hydrolase C11orf54 homolog [ACO11749; *Caligus rogercresseyi*] (*Salmo salar* feature)	156 (99%)	3E-86	Hydrolase activity, acting on ester bonds; Zinc ion binding (GO:0016788; GO:0008270) [C1BRU6]	5.389	1.681
CB516671	Ester hydrolase C11orf54 homolog [ACO11749; *Caligus rogercresseyi*] (*Salmo salar* feature)	160 (100%)	1E-90	Hydrolase activity, acting on ester bonds; Zinc ion binding (GO:0016788; GO:0008270) [C1BRU6]	3.842	0.582
CB514052	Extra spindle poles-like 1 [AAI45845; *Mus musculus*]	144 (35%)	1E-17	Peptidase activity (GO:0008233) [A6H6E1]	2.455	0.421
CB516919	Extracellular matrix protein 1 precursor [ACN10906; *Salmo salar*] (*Salmo salar* type 1)	97 (97%)	3E-48	Extracellular space (GO:0005615) [C0HA37] [c]	2.519	0.118
CA038043	Extracellular matrix protein 1 precursor [BT059193; *Salmo salar*] [N] (*Salmo salar* type 2)	587 (84%)	3E-141	Extracellular space (GO:0005615) [C0HA37] [c]	3.248	0.497
CA040448	Extracellular matrix protein 1 precursor [BT059193; *Salmo salar*] [N] (*Salmo salar* type 3)	568 (99%)	0	Extracellular space (GO:0005615) [C0HA37] [c]	2.060	0.186

CB498116	Fast myotomal muscle troponin-T-1 [ACH71024; *Salmo salar*]	72 (100%)	2E-26	Unknown	3.997	0.619
CK990311	Fat-inducing transcript 1 [AAH90787; *Danio rerio*]	106 (86%)	6E-31	Endoplasmic reticulum membrane; Integral to membrane (GO:0005789; GO:0016021) [Q5CZN0] [c]	5.112	2.047
CB489347	Fatty acid binding protein H-FABP [AAB53643; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	133 (100%)	1E-68	Lipid binding; Transporter activity (GO:0008289; GO:0005215) [O13008]	28.201	19.129
CB492969	Fatty acid binding protein H-FABP [AAB53643; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	133 (100%)	1E-68	Lipid binding; Transporter activity (GO:0008289; GO:0005215) [O13008]	7.126	2.484
CB486281	Ferritin heavy subunit [AAB34575; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	120 (94%)	3E-65	Ferric iron binding; Ferroxidase activity (GO:0008199; GO:0004322) [P49946]	6.405	1.419
CB489257	Ferritin heavy subunit [AAB34575; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	139 (99%)	2E-76	Ferric iron binding; Ferroxidase activity (GO:0008199; GO:0004322) [P49946]	4.218	0.707
CB493178	Ferritin-H subunit [AAK08117|AF338763; *Oncorhynchus nerka*]	65 (95%)	8E-57	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [Q98TT0]	5.339	1.186
CB509708	Ferritin, heavy polypeptide 1-1 [ACH70933; *Salmo salar*]	127 (97%)	6E-69	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5DGQ9]	3.783	0.654
CB496534	Ferritin, heavy subunit [ACO07472; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* type 2)	75 (92%)	2E-75	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [C1BEL9]	3.931	0.720
CB498077	Ferritin, heavy subunit [ACO07472; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss*	126 (100%)	3E-86	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [C1BEL9]	6.836	0.797

	type 2)					
CB499529	Ferritin, heavy subunit [BT059031; *Salmo salar*] [(N)] (*Salmo salar* type 1)	615 (99%)	0	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5DGQ9]	2.119	0.142
CB510588	Ferritin, heavy subunit [BT059031; *Salmo salar*] [(N)] (*Salmo salar* type 2)	61 (94%)	2E-14	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [B5DGQ9]	6.463	2.508
CB487639	Ferritin, middle subunit [ACI66713; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	130 (95%)	1E-66	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5X793]	17.889	2.532
CB503780	Ferritin, middle subunit [ACI68639; *Salmo salar*] (*Salmo salar* feature)	162 (100%)	4E-89	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5XCR9]	4.349	0.823
CA042437	Ferritin, middle subunit [ACI68920; *Salmo salar*] (*Salmo salar* feature) (FTM, Fig. 11D)	70 (100%)	6E-34	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5XDK0]	3.432	0.321
CB502663	Ferritin, middle subunit [ACI69419; *Salmo salar*] (*Salmo salar* feature) (FTM, Fig. 11D)	145 (99%)	9E-79	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5XEZ9]	2.472	0.462
CB505282	Ferritin, middle subunit [ACI69640; *Salmo salar*] (*Salmo salar* feature) (FTM, Fig. 11D)	105 (99%)	1E-72	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [B5XFM0]	3.628	0.549
CB510731	Ferritin, middle subunit [ACO07744; *Oncorhynchus mykiss*] (*Salmo salar* feature) (Fig. 11D)	124 (100%)	3E-66	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [C1BFE1]	2.508	0.432
CB498370	Ferritin, middle subunit [ACO08179; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* type 2)	113 (100%)	2E-59	Ferric iron binding; Oxidoreductase activity (GO:0008199; GO:0016491) [C1BGM6]	3.787	0.609
CB497894	Fibrinogen beta chain precursor [ABJ98546; *Larimichthys*	491 (71%)/	0/0	Protein binding, bridging; Receptor binding (GO:0030674; GO:0005102)	2.278	0.146

	crocea]/[EZ905536; *Oncorhynchus mykiss*] [(B)]	574 (99%)		[A0FJG5]		
EG842506	Forkhead box protein Q1 [ACO13697; *Esox lucius*]	192 (86%)	8E-95	Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity (GO:0043565; GO:0003700) [C1BXE4]	13.788	11.493
CA050412	Foxl2-like protein [HM159472; *Salmo salar*] [(N)]	407 (83%)	2E-82	Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity (GO:0043565; GO:0003700) [E3UBG6]	5.284	2.444
CB496932	Fructose-1,6-bisphosphatase [ACH70893; *Salmo salar*]	190 (97%)	2E-119	Fructose 1,6-bisphosphate 1-phosphatase activity (GO:0042132) [B5DGL9]	14.334	11.028
CA037915	Fumarylacetoacetase [ACO09168; *Osmerus mordax*] (*Salmo salar* type 1)	137 (88%)	1E-69	Fumarylacetoacetase activity (GO:0004334) [C1BJG5]	2.806	0.462
CA054963	Galactosamine (N-acetyl)-6-sulfate sulfatase [AAI29219; *Danio rerio*]	72 (75%)	5E-29	Sulfuric ester hydrolase activity (GO:0008484) [A1L1U7]	6.556	4.567
CB493525	Gastric chitinase [ACG58867; *Oncorhynchus mykiss*]	122 (100%)	4E-57	Cation binding; Chitin binding; Chitinase activity (GO:0043169; GO:0008061; GO:0004568) [B5AXN7]	2.017	0.280
CB510239	General transcription factor IIH subunit 5 [ACI67115; *Salmo salar*]	71 (100%)	2E-32	DNA binding (GO:0003677) [B5X8E5]	6.156	2.907
CB510360	Glucose-6-phosphatase [ABC49921; *Chanodichthys ilishaeformis*]	43 (87%)	3E-12	Catalytic activity (GO:0003824) [Q2MJT2]	2.050	0.206
CB496429	Glutamate dehydrogenase [AJ556998; *Oncorhynchus mykiss*] [(N)] (*Oncorhynchus mykiss* feature)	694 (99%)	0	Binding; Glutamate dehydrogenase [NAD(P)+] activity (GO:0005488; GO:0004353) [Q70PJ5]	2.861	0.745
CA053189	Glutamate dehydrogenase 1,	515	0	Binding; Oxidoreductase activity, acting	2.290	0.249

	mitochondrial precursor [BT044837; *Salmo salar*] (N) (*Salmo salar* feature)	(100%)		on the CH-NH2 group of donors, NAD or NADP as acceptor (GO:0005488; GO:0016639) [B5X1B8]		
CB493171	Glutamine synthetase [AAM73660|AF390022; *Oncorhynchus mykiss*]	78 (100%)	1E-38	ATP binding; Glutamate-ammonia ligase activity (GO:0005524; GO:0004356) [Q8JI33]	33.222	10.108
CB509722	Glutathione peroxidase 3 precursor [BT072794; *Salmo salar*] (N)	492 (99%)	0	Unknown	3.956	1.053
CB494587	Glutathione peroxidase type 2 [AAV32968; *Oncorhynchus mykiss*]	71 (85%)	1E-28	Glutathione peroxidase activity (GO:0004602) [Q5UTE7]	2.436	0.339
CB497579	Glutathione S-transferase [BAA76974; *Oncorhynchus nerka*]	159 (97%)	3E-84	Glutathione transferase activity (GO:0004364) [Q9W647]	10.755	2.241
CB492604	Glutathione S-transferase A [ACO07597; *Oncorhynchus mykiss*]	48 (98%)	5E-19	Transferase activity (GO:0016740) [C1BEZ4]	14.635	11.620
CA044880	Glutathione S-transferase theta-1 [ACI33850; *Salmo salar*]	155 (100%)	6E-83	Transferase activity (GO:0016740) [B5X3G9]	20.463	16.928
CB492813	Glyceraldehyde-3-phosphate dehydrogenase [ACI33883; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	113 (100%)	5E-54	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X3K2]	17.508	6.500
CA051897	Glyceraldehyde-3-phosphate dehydrogenase [ACI33883; *Salmo salar*] (*Salmo salar* type 3)	123 (100%)	3E-59	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X3K2]	3.727	0.789
CB498361	Glyceraldehyde-3-phosphate dehydrogenase [ACI66269; *Salmo salar*] (*Oncorhynchus mykiss* type 2)	146 (99%)	5E-78	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X5Z9]	4.953	1.826

BU965756	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*] (*Salmo salar* type 2) (GAPDH2, Fig. 13B)	116 (100%)	3E-60	NAD binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]	26.555	14.650
CA041846	Glycoprotein 2 [EAW50313; *Homo sapiens*]/[EZ864353; *Oncorhynchus mykiss*] (B)	72 (44%)/ 191 (96%)	7E-10/ 2E-80	Unknown	3.508	0.282
CA041207	Golgi-associated plant pathogenesis-related protein 1 [BT045651; *Salmo salar*] (N)	558 (95%)	0	Extracellular region (GO:0005576) [B5X3N2] [c]	6.321	2.007
CA043115	Guanine nucleotide-protein beta-4 subunit [AAF82124; *Mus musculus*] (G)	340 (86%)	1.3E-24	Signal transducer activity (GO:0004871) [P29387]	2.695	0.436
CB497009	Heat shock 70kDa protein 8 [AAQ97970; *Danio rerio*] (X)	94 (91%)	5E-43	ATP binding (GO:0005524) [Q6TEQ5]	2.661	0.266
CB493960	Heat shock 90kDa protein 1 beta isoform b [BAD90024; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	59 (100%)	1E-26	ATP binding; Unfolded protein binding (GO:0005524; GO:0051082) [Q5DW65]	3.387	0.710
EG860968	Heat shock 90kDa protein 1 beta isoform b [BAD90024; *Oncorhynchus mykiss*] (*Salmo salar* feature)	204 (99%)	3E-98	ATP binding; Unfolded protein binding (GO:0005524; GO:0051082) [Q5DW65]	7.833	4.461
EG884321	Heat shock cognate 70 kDa protein [ACN11074; *Salmo salar*]	109 (100%)	4E-56	ATP binding (GO:0005524) [C0HAK5]	2.761	0.623
CB498852	Heat shock cognate 71 kDa protein [AAB21658; *Oncorhynchus mykiss*]	207 (100%)	4E-114	ATP binding (GO:0005524) [P08108]	2.586	0.216
EG813231	Heat shock protein 70 isoform 3 [ACH70704; *Salmo salar*]	111 (100%)	1E-56	ATP binding (GO:0005524) [B5DG30]	17.297	10.015

CB502683	Heat shock protein 8 [AAH63228; *Danio rerio*] (X)	173 (95%)	8E-89	ATP binding (GO:0005524) [Q6NYR4]	8.541	1.562
CA044621	Hemagglutinin/amebocyte aggregation factor precursor [ACI68653; *Salmo salar*]	117 (78%)	8E-56	Unknown	3.066	0.397
CB493961	Hemoglobin subunit alpha [ACI69100; *Salmo salar*] (*Oncorhynchus mykiss* feature)	143 (99%)	4E-74	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XE30]	2.969	0.246
CB497564	Hemoglobin subunit alpha [ACI69100; *Salmo salar*] (*Salmo salar* feature)	143 (99%)	9E-74	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XE30]	4.324	1.230
CB498419	Hemoglobin subunit alpha-1 [ACO07570; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	143 (100%)	8E-76	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [Q98974]	4.064	0.468
CB497309	Hemoglobin subunit beta-4 [ACO07576; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	148 (100%)	6E-80	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BEX3]	4.085	0.673
CB497723	Hemoglobin subunit beta-4 [ACO08020; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	148 (99%)	2E-78	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BG67]	3.639	1.223
CB498665	Hemoglobin subunit beta-4 [ACO08020; *Oncorhynchus mykiss*]	148 (100%)	5E-80	Heme binding; Oxygen binding; Oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BG67]	2.435	0.504
CB497659	Heparin cofactor II [AAN71003|AF515273; *Danio rerio*]/[EZ764595; *Oncorhynchus mykiss*] (B) (X)	304 (80%)/ 571 (99%)	1E-174/ 0	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q8AYE2]	9.872	3.180
DW541676	Hepatocyte nuclear factor 4 alpha [AAH56550; *Danio rerio*] (G)	463 (94%)	2E-119	Sequence-specific DNA binding; Sequence-specific DNA binding	3.194	0.737

				transcription factor activity; Steroid hormone receptor activity; Zinc ion binding (GO:0043565; GO:0003700; GO:0003707; GO:0008270) [Q6PHH5]		
CA042004	High affinity copper uptake protein 1 [ACN11071; *Salmo salar*]	114 (84%)	4E-47	Copper ion transmembrane transporter activity (GO:0005375) [C0HAK2]	2.748	0.325
CB498109	High-mobility group 20B [AAH95120; *Danio rerio*]	117 (86%)	1E-48	DNA binding (GO:0003677) [Q503Z1]	2.982	0.520
CA062128	Histone deacetylase 2 [BT045315; *Salmo salar*] (N)	619 (99%)	0	Histone deacetylase activity (GO:0004407) [B5X2P6]	2.307	0.420
CB510848	Histone H1.0 [ACN10192; *Salmo salar*]	82 (100%)	3E-42	DNA binding (GO:0003677) [C0H823]	12.891	7.251
CA055883	Homogentisate 1,2-dioxygenase [AAI52650; *Danio rerio*] (X)	78 (84%)	4E-34	Homogentisate 1,2-dioxygenase activity (GO:0004411) [Q6P2V4]	2.063	0.173
CA369758	Inhibitor of DNA binding/differentiation 1D [AAX46287; *Oncorhynchus mykiss*]	126 (100%)	1E-65	Transcription regulator activity (GO:0030528) [Q4VKK4]	6.110	3.946
CA043333	Inositol 1,4,5-trisphosphate 3-kinase A [BC123676; *Bos taurus*] (N)	197 (77%)	4E-17	Inositol trisphosphate 3-kinase activity (GO:0008440) [A4FV33]	2.606	0.634
CA037863	Inositol-trisphosphate 3-kinase A [DAA25447; *Bos taurus*]	112 (60%)	2E-29	Unknown	2.616	0.204
CA347369	Intelectin 2 [ACC62157; *Danio rerio*]	168 (71%)	2E-70	Receptor binding (GO:0005102) [C1IHV0]	8.082	3.472
CA057269	Intraflagellar transport 52 homolog [ACO09308; *Osmerus mordax*]	131 (94%)	1E-55	Flagellum (GO:0019861)[C1BJV5] [c]	2.736	0.475
CB498181	Kelch repeat and BTB (POZ) domain containing 10	76 (96%)	5E-35	Unknown	4.020	1.000

	[ACH70794; *Salmo salar*]					
CB493926	Keratin 18, simple type I keratin [CAA74664; *Oncorhynchus mykiss*]	73 (100%)	5E-24	Structural molecule activity (GO:0005198) [O57607]	7.347	2.658
CB496780	Kif1-binding protein [ABW89743; *Danio rerio*] (*Oncorhynchus mykiss* feature)	67 (73%)	2E-10	Binding (GO:0005488) [A8WE67]	6.078	0.706
DY722735	Kif1-binding protein [ABW89743; *Danio rerio*]/[EZ853027; *Oncorhynchus mykiss*] [(B)] (*Salmo salar* feature)	74 (79%)/ 489 (94%)	8E-26/ 0	Binding (GO:0005488) [A8WE67]	2.048	0.262
CB494268	Kininogen-1 precursor [ACO13619; *Esox lucius*] (*Oncorhynchus mykiss* feature)	154 (57%)	1E-35	Cysteine-type endopeptidase inhibitor activity (GO:0004869) [C1BX66]	2.860	0.284
CB497601	Kininogen-1 precursor [ACO13619; *Esox lucius*] (*Oncorhynchus mykiss* feature)	184 (60%)	2E-49	Cysteine-type endopeptidase inhibitor activity (GO:0004869) [C1BX66]	4.787	0.693
CA037891	Leukocyte cell-derived chemotaxin 2 [ABD16188; *Danio rerio*] [(X)]	55 (84%)	1E-20	Response to bacterium (GO:0009617) [Q0H0R9] [b]	3.630	0.635
CB497217	Leukocyte elastase inhibitor [ACI34221; *Salmo salar*]	136 (88%)	7E-57	Serine-type endopeptidase inhibitor activity (GO:0004867) [B5X4J0]	4.132	0.757
CB509870	Lipocalin precursor [ACI68588; *Salmo salar*] (*Salmo salar* type 2)	136 (100%)	1E-74	Binding; Transporter activity (GO:0005488; GO:0005215) [B5XCL8]	2.989	0.537
CA043176	Lipocalin precursor [ACI69895; *Salmo salar*] (*Salmo salar* type 1)	84 (100%)	1E-41	Binding; Transporter activity (GO:0005488; GO:0005215) [B5XGC5]	4.045	0.738
CB510500	Lipocalin precursor [ACI69895; *Salmo salar*] (*Salmo salar* type	151 (93%)	1E-74	Binding; Transporter activity (GO:0005488; GO:0005215) [B5XGC5]	9.269	1.680

	1)					
CB511307	Lipocalin precursor [ACI69895; *Salmo salar*] (*Salmo salar* type 1)	137 (100%)	3E-74	Binding; Transporter activity (GO:0005488; GO:0005215) [B5XGC5]	2.737	0.284
CB492836	Lipocalin precursor [ACI70053; *Salmo salar*] (*Oncorhynchus mykiss* type 1)	147 (99%)	5E-81	Binding; Transporter activity (GO:0005488; GO:0005215) [B5XGT3]	12.738	9.667
CB509536	Lipocalin precursor [ACQ58872; *Anoplopoma fimbria*]/[EZ774133; *Oncorhynchus mykiss*] [(B)] (*Salmo salar* type 3)	71 (48%)/ 179 (98%)	1E-18/ 7E-79	Binding; Transporter activity (GO:0005488; GO:0005215) [C3KJQ0]	2.526	0.265
CB493980	Lipocalin precursor [BT125535; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* type 2)	216 (89%)	7E-64	Binding; Transporter activity (GO:0005488; GO:0005215) [B5XCL8]	2.480	0.421
CK990953	Liver-basic fatty acid binding protein b [ACA64701; *Cyprinus carpio*]	126 (84%)	4E-55	Lipid binding; Transporter activity (GO:0008289; GO:0005215) [B3FQT5]	2.286	0.454
CA387966	Liver-expressed antimicrobial peptide 2B [AAR11767; *Oncorhynchus mykiss*]	90 (99%)	7E-47	Defense response to bacterium (GO:0042742) [Q64JE5] [b]	4.205	0.292
DW556988	Low density lipoprotein receptor-related protein 1 [EAW96990; *Homo sapiens*]	54 (62%)	2E-11	Unknown	2.504	0.479
CA044851	LYR motif-containing protein 5 [ACI67205; *Salmo salar*]	36 (87%)	3E-12	Unknown	19.298	13.615
CB511680	Lysozyme C II precursor [ACI67735; *Salmo salar*]	95 (99%)	1E-51	Lysozyme activity (GO:0003796) [B5XA65]	2.335	0.282
CA048910	Macrosialin precursor [BT058906; *Salmo salar*] [(N)]	633 (99%)	0	Membrane (GO:0016020) [C0H9A0] [c]	12.645	7.089
CB493204	Malate dehydrogenase 2-1, NAD	102 (99%)	9E-86	L-malate dehydrogenase activity; binding	3.014	0.572

	(mitochondrial) [ACH70948; *Salmo salar*] (*Oncorhynchus mykiss* feature)			(GO:0030060; GO:0005488) [B5DGS4]		
CA042642	Malate dehydrogenase, mitochondrial precursor [ACI66104; *Salmo salar*] (*Oncorhynchus mykiss* feature)	130 (100%)	6E-66	L-malate dehydrogenase activity; binding (GO:0030060; GO:0005488) [B5X5I4]	4.501	0.540
CB497871	Malate dehydrogenase, cytoplasmic (MDH) gene [HQ287747; *Coregonus clupeaformis*] [(N)] (*Oncorhynchus mykiss* type 1)	406 (91%)	7E-149	Unknown	14.201	6.983
CB509929	Malate dehydrogenase, cytoplasmic (MDH) gene [HQ287747; *Coregonus clupeaformis*] [(N)] (*Salmo salar* type 1)	185 (91%)	5E-60	Unknown	2.168	0.264
EG834633	Malate dehydrogenase, cytoplasmic (MDH) gene [HQ287747; *Coregonus clupeaformis*] [(N)] (*Salmo salar* type 2)	140 (90%)	1E-41	Unknown	3.236	0.780
CB493498	Malate dehydrogenase, cytoplasmic [ACN10417; *Salmo salar*] (*Oncorhynchus mykiss* type 2)	107 (100%)	5E-61	L-malate dehydrogenase activity; binding (GO:0030060; GO:0005488) [C0H8P8]	4.535	0.712
EG873759	Membrane-bound transcription factor protease, site 1 [CAK04389; *Danio rerio*] (*Salmo salar* type 1)	202 (94%)	7E-110	Serine-type endopeptidase activity (GO:0004252) [Q1LWH3]	2.320	0.109
CA060233	Membrane-bound transcription factor protease, site 1 [CAK04389; *Danio rerio*]	75 (90%)	2E-15	Serine-type endopeptidase activity (GO:0004252) [Q1LWH3]	2.139	0.399

	(*Salmo salar* type 2)					
EG825034	Membrane-spanning 4-domains subfamily A member 4A [ACI69003; *Salmo salar*]	139 (41%)	1E-14	Integral to membrane (GO:0016021) [B5XDT3] [c]	6.279	2.702
CB510653	Metallothionein B [AY267818; *Salvelinus alpinus*] [(N)]	536 (85%)	8E-134	Metal ion binding (GO:0046872) [P68502]	9.424	5.703
CB508872	Metallothionein-A [AF098071; *Salvelinus alpinus*] [(N)]	369 (98%)	7E-174	Metal ion binding (GO:0046872) [P68505]	7.179	1.286
CA048859	MHC Class I (Sasa-UBA) [EF210363; *Salmo salar*] [(N)]	566 (99%)	0	MHC class I protein complex (GO:0042612) [A7KDZ8] [c]	2.618	0.278
CA043995	MHC class I a region [AB162342; *Oncorhynchus mykiss*] [(N)]	207 (94%)	7E-79	MHC class I protein complex (GO:0042612) [Q5FBU0] [c]	2.614	0.477
CA044961	Mu-crystallin homolog [ACM08876; *Salmo salar*]	149 (100%)	5E-79	Binding; Catalytic activity (GO:0005488; GO:0003824) [B9EMX9]	2.415	0.414
CB497206	Myelin basic protein [AAW52552; *Danio rerio*]/[EZ764180; *Oncorhynchus mykiss*] [(B)]	89 (44%)/ 44 (100%)	1E-05/ 4E-12	Structural constituent of myelin sheath (GO:0019911) [Q5I2C7]	16.938	11.593
CB517843	Myelin protein zero-like protein 2 precursor [ACI67989; *Salmo salar*] (*Salmo salar* type 1)	46 (68%)	3E-11	Membrane (GO:0016020) [B5XAW9] [c]	6.153	2.891
EG855765	Myelin protein zero-like protein 2 precursor [ACI67989; *Salmo salar*] (*Salmo salar* type 2)	54 (67%)	7E-12	Membrane (GO:0016020) [B5XAW9] [c]	2.529	0.371
CB505582	Myristoylated alanine-rich C-kinase substrate [BT045958; *Salmo salar*] [(N)]	630 (100%)	0	Calmodulin binding; kinase activity (GO:0005516; GO:0016301) [B5X4I9]	2.303	0.327
CB490998	N2,N2-dimethylguanosine tRNA methyltransferase [ACN11277; *Salmo salar*]	126 (98%)	3E-69	RNA binding; tRNA (guanine-N2-)-methyltransferase activity; Zinc ion binding (GO:0003723; GO:0004809; GO:0008270) [C0HB58]	3.904	1.159

CA044305	NADH dehydrogenase 1 alpha subcomplex subunit 4 [ACM08519; *Salmo salar*] (*Salmo salar* feature)	81 (100%)	6E-42	Unknown	4.443	1.821
CB489039	NADH dehydrogenase 1 alpha subcomplex subunit 4 [ACO08391; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	42 (96%)	7E-20	Unknown	33.515	11.111
CB498084	NADH dehydrogenase 1 alpha subcomplex subunit 4 [ACO08391; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	81 (100%)	2E-41	Unknown	4.614	1.400
EG848419	NADH dehydrogenase iron-sulfur protein 5 [ACI68144; *Salmo salar*]	107 (99%)	3E-59	Unknown	3.471	0.812
CB494566	Nascent polypeptide-associated complex alpha polypeptide [AAM21714; *Danio rerio*] (X) (*Oncorhynchus mykiss* type 1)	109 (99%)	8E-38	Cytoplasm; Nucleus (GO:0005737; GO:0005634) [Q8JIU7] [c]	9.862	6.710
CK991355	Nascent polypeptide-associated complex alpha polypeptide [AAM21714; *Danio rerio*] (X) (*Oncorhynchus mykiss* type 2)	109 (99%)	8E-38	Cytoplasm; Nucleus (GO:0005737; GO:0005634) [Q8JIU7] [c]	2.315	0.355
CA366949	Nascent polypeptide-associated complex subunit alpha [BT074369; *Oncorhynchus mykiss*] (N) (*Oncorhynchus mykiss* type 3)	107 (100%)	2E-47	Unknown	4.810	1.302
CB505581	Non-muscle actin [EFW40167; *Capsaspora owczarzaki*]	42 (100%)	5E-17	Unknown	3.331	0.913

CB494512	Nonhistone chromosomal protein H6 [BT074292; *Oncorhynchus mykiss*] [(N)]	542 (100%)	0	DNA binding (GO:0003677) [C1BFL7]	16.408	6.196
DW563838	Novel KRAB box and zinc finger, C2H2 type domain containing protein [CAM27169; *Mus musculus*]	113 (61%)	4E-36	Nucleic acid binding; Zinc ion binding (GO:0003676; GO:0008270) [A2BG91]	2.256	0.419
CA057076	Novel protein similar to vertebrate cyclic nucleotide gated channel protein family [CAX14661; *Danio rerio*]	171 (77%)	3E-62	Ion channel activity (GO:0005216) [B8JHY6]	2.246	0.472
EG873384	Novel protein similar to vertebrate ring finger protein 10 [CAQ13329; *Danio rerio*]/[BT072433; *Salmo salar*] [(B)]	49 (74%)/ 747 (99%)	3E-12/ 0	Zinc ion binding (GO:0008270) [B0UXR5]	2.354	0.438
CB504059	Novel protein similar to vertebrate solute carrier (sodium-coupled nucleoside transporter) family 28 [CAK10822; *Danio rerio*] [(X)]	75 (55%)	1E-16	Nucleoside binding; Nucleoside:sodium symporter activity (GO:0001882; GO:0005415) [Q1LX55]	3.284	0.226
CB490586	Nuclear protein 1 [AAH02109; *Mus musculus*] [(X)] (*Oncorhynchus mykiss* feature) (NUPR1, Fig. 11E)	57 (56%)	4E-11	Nucleus (GO:0005634) [Q9WTK0] [c]	185.550	50.854
CB507001	Nuclear protein 1 [AAH02109; *Mus musculus*] [(X)] (*Salmo salar* type 1) (*Salmo salar* type 1)	59 (56%)	1E-8	Nucleus (GO:0005634) [Q9WTK0] [c]	2.030	0.334
CB497385	Nuclear protein 1 [BT048359; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* feature)	552 (90%)	0	Unknown	5.799	0.733
EG898351	Nuclear protein 1 [BT048359; *Salmo salar*] [(N)] (*Salmo salar*	697 (90%)	0	Unknown	6.678	0.910

	type 2)					
CA044682	Nuclear protein 1 [BT056591; *Salmo salar*] [(N)] (*Salmo salar* type 3)	219 (100%)	2E-109	Unknown	3.209	0.478
CA044994	Nuclear receptor subfamily 5, group A, member 5 [AAI63909; *Danio rerio*]	77 (88%)	5E-32	Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity; Steroid hormone receptor activity; Zinc ion binding (GO:0043565; GO:0003700; GO:0003707; GO:0008270) [B3DKN2]	4.103	1.590
CB510514	Nucleoside diphosphate kinase [ACM80355; *Oncorhynchus mykiss*]	165 (98%)	2E-90	ATP binding; Nucleoside diphosphate kinase activity (GO:0005524; GO:0004550) [C0KIP7]	3.132	0.134
CB510537	Nucleoside diphosphate kinase A [ACI68568; *Salmo salar*]	139 (100%)	2E-76	ATP binding; Nucleoside diphosphate kinase activity (GO:0005524; GO:0004550) [B5XCJ8]	3.339	0.324
CB498087	OCIA domain-containing protein 2 [ACI69700; *Salmo salar*]	145 (81%)	5E-47	Unknown	4.064	0.350
CA045168	Olfactomedin 4 [AAH47740; *Homo sapiens*]	137 (53%)	6E-36	Extracellular space (GO:0005615) [Q6UX06] [c]	3.661	1.799
CB493774	Ornithine decarboxylase antizyme small isoform [AAP82032; *Paralichthys olivaceus*]	43 (96%)	1E-23	Ornithine decarboxylase inhibitor activity (GO:0008073) [Q6X3F2]	3.581	1.118
CA037720	Orphan nuclear receptor SHP [AAN17673; *Oreochromis niloticus*]	193 (61%)	2E-57	DNA binding; Sequence-specific DNA binding transcription factor activity; Steroid hormone receptor activity (GO:0003677; GO:0003700; GO:0003707) [Q8AUM4]	22.511	18.968
CB497819	Pancreatic progenitor cell differentiation and proliferation factor b [ADO28364; *Ictalurus furcatus*] (*Oncorhynchus mykiss*	73 (72%)	2E-20	Unknown	2.380	0.438

	feature)					
EG782703	Pancreatic progenitor cell differentiation and proliferation factor b [ADO28849; *Ictalurus punctatus*] (*Salmo salar* feature)	115 (63%)	8E-26	Unknown	29.867	20.553
CB498239	Peptidylarginine deiminase [CAX45844; *Oncorhynchus mykiss*]	157 (100%)	3E-87	Calcium ion binding; Protein-arginine deiminase activity (GO:0005509; GO:0004668) [B9WPX5]	2.937	0.196
CA052837	Phosphoglycerate mutase 1 [BT044637; *Salmo salar*] (N)	732 (99%)	0	2,3-Bisphosphoglycerate-dependent phosphoglycerate mutase activity (GO:0046538) [B5X0R8]	2.555	0.364
EG813037	Phytanoyl-CoA dioxygenase, peroxisomal precursor [ACI33694; *Salmo salar*]	112 (87%)	3E-52	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen (GO:0016702) [B5X313]	8.313	1.999
CA038535	Plasminogen [CAD69012; *Oncorhynchus mykiss*] (*Salmo salar* feature)	160 (93%)	2E-72	Serine-type endopeptidase activity (GO:0004252) [Q5DVP8]	4.166	0.882
CB494600	Plasminogen [CAD69012; *Oncorhynchus mykiss*] (*Oncorhynchus mykiss* feature)	227 (85%)	5E-114	Serine-type endopeptidase activity (GO:0004252) [Q5DVP8]	3.858	0.968
CA053675	Platelet glycoprotein V precursor [BT072396; *Salmo salar*] (N)	672 (99%)	0	Unknown	4.188	2.008
CB493634	Polyprotein [ABA54982; Atlantic salmon swim bladder sarcoma virus]/[EZ905132; *Oncorhynchus mykiss*] (B)	301 (83%)/ 717 (98%)	0/0	DNA binding; RNA binding; RNA-directed DNA polymerase activity; Aspartic-type endopeptidase activity; Ribonuclease H activity; Zinc ion binding (GO:0003677; GO:0003723; GO:0003964; GO:0004190; GO:0004523; GO:0008270) [Q2VF30]	9.088	2.422
DY741061	POU domain, class 4, transcription factor 2	157 (97%)	4E-72	Sequence-specific DNA binding; Sequence-specific DNA binding	2.858	0.733

	[ACN10506; *Salmo salar*]			transcription factor activity; Transcription regulator activity (GO:0043565; GO:0003700; GO:0030528) [C0H8Y7]		
CB509563	Pre-mRNA-splicing factor 18 [ACO09138; *Osmerus mordax*]/[EZ871571; *Oncorhynchus mykiss*] [(B)] (*Salmo salar* feature)	247 (55%)/ 513 (88%)	3E-86/ 3E-161	Spliceosomal complex (GO:0005681) [C1BJD5] [c]	7.663	2.720
CB497341	Precerebellin-like protein [AAF04305|AF192969; *Oncorhynchus mykiss*]	186 (86%)	5E-71	Unknown	3.313	0.558
CA042490	Prefoldin subunit 3 [BT072072; *Salmo salar*] [(N)]	102 (90%)	6E-25	Unfolded protein binding (GO:0051082) [C0PU61]	2.391	0.311
CK991353	Prepro-cathepsin C [AY593996; *Oncorhynchus mykiss*] [(N)]	634 (97%)	0	Cysteine-type endopeptidase activity (GO:0004197) [Q64HY0]	2.517	0.398
CA038358	Proteasome subunit alpha type 2 [ACO08660; *Oncorhynchus mykiss*]	106 (100%)	3E-55	Threonine-type endopeptidase activity (GO:0004298) [C1BI07]	7.218	3.866
CB491335	Protein CARP-like protein [EFN79817; *Harpegnathos saltator*] [(X)]	163 (34%)	1E-13	Calcium ion binding (GO:0005509) [E2BWV3]	2.301	0.243
CA044554	Prothymosin, alpha a [AAH68334; *Danio rerio*] [(X)] (*Salmo salar* type 1)	36 (89%)	4E-8	Nucleus (GO:0005634) [Q6NV32] [c]	22.766	15.157
EG877115	Pterin-4-alpha-carbinolamine dehydratase [ACM08306; *Salmo salar*]	102 (100%)	2E-52	4-Alpha-hydroxytetrahydrobiopterin dehydratase activity (GO:0008124) [B9ELA9]	14.872	6.574
CB493802	Pyruvate dehydrogenase complex, component X [AAH61231; *Mus musculus*]/[EZ906063; *Oncorhynchus mykiss*] [(B)]	71 (65%)/ 545 (99%)	3E-15/0	Acyltransferase activity (GO:0008415) [Q8BKZ9]	3.370	0.296

FC072716	Ras-related protein Rab-1A [BT059362; *Salmo salar*] [(N)]	352 (99%)	2E-173	GTP binding (GO:0005525) [C0HAK6]	2.821	0.493
CA055402	Receptor for activated protein kinase C [AAB81617; *Danio rerio*] [(X)] (*Salmo salar* feature)	174 (96%)	4E-110	Angiogenesis (GO:0001525) [O42248] [b]	3.206	0.318
CB493280	Receptor for activated protein kinase C [AAB81617; *Danio rerio*] [(X)] (*Oncorhynchus mykiss* type 1)	174 (96%)	4E-110	Angiogenesis (GO:0001525) [O42248] [b]	2.555	0.156
CB497163	Receptor for activated protein kinase C [AAB81617; *Danio rerio*] [(X)] (*Oncorhynchus mykiss* type 2)	174 (96%)	4E-110	Angiogenesis (GO:0001525) [O42248] [b]	7.095	0.798
CB497413	Reproduction regulator 2 [AAN02165; *Epinephelus coioides*]	110 (40%)	1E-13	Unknown	23.168	13.391
CB492868	RER1 retention in endoplasmic reticulum 1 [BT045447; *Salmo salar*] [(N)]	160 (80%)	8E-18	Integral to membrane (GO:0016021) [B5X328] [c]	3.912	1.725
CB498195	Reticulon 4 [BK004986; *Oncorhynchus mykiss*] [(N)]	637 (99%)	0	Endoplasmic reticulum (GO:0005783) [Q4FZ68]	3.779	0.886
DW543479	Retinoic acid receptor gamma b [EU025716; *Salmo salar*] [(N)]	391 (86%)	5E-100	Retinoic acid receptor activity; Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity; Steroid hormone receptor activity; Zinc ion binding (GO:0003708; GO:0043565; GO:0003700; GO:0003707; GO:0008270) [B3TDG8]	2.841	1.010
CA050645	Retinoic acid receptor responder protein 3 [ACI69191; *Salmo salar*]	27 (100%)	7E-7	Receptor activity (GO:0004872) [B5XEC1]	3.059	0.654
CB492550	Retinol-binding protein	139	3E-80	Retinoid binding; Transporter activity	3.629	0.883

	[AAL14872; *Oncorhynchus mykiss*]	(100%)		(GO:0005501; GO:0005215) [Q90Y51]		
CB496593	Retinol-binding protein 2 [ADO29353; *Ictalurus punctatus*]	135 (71%)	1E-51	Lipid binding; Transporter activity (GO:0008289; GO:0005215) [E3TGB7]	4.406	1.463
CA038814	Reverse transcriptase [AAS83200; *Fundulus heteroclitus*] (*Salmo salar* feature) (*Salmo salar* feature)	115 (29%)	9E-9	RNA binding; RNA-directed DNA polymerase activity (GO:0003723; GO:0003964) [Q64IX6]	3.875	0.535
CB493524	Reverse transcriptase-like protein [AAN15747; *Paralichthys olivaceus*]/[CU627990; *Danio rerio*] [(B)] (*Oncorhynchus mykiss* feature)	160 (69%)/ 52 (89%)	5E-57/ 1E-05	RNA binding; RNA-directed DNA polymerase activity (GO:0003723; GO:0003964) [Q7T271]	2.695	0.580
EG929833	Rho GTPase activating protein 11A [AAH63444; *Homo sapiens*] [(X)]	116 (48%)	3E-18	GTPase activator activity (GO:0005096) [Q6P4F7]	2.513	0.477
CB498444	Ribosomal protein L12 [ACH70859; *Salmo salar*]	165 (100%)	2E-88	Structural constituent of ribosome (GO:0003735) [B5DGI5]	2.796	0.367
CA062778	Ribosomal protein L19 [BT043693; *Salmo salar*] [(N)]	148 (100%)	6E-70	Structural constituent of ribosome (GO:0003735) [B5DGD4]	3.560	0.654
CA038333	Ribosomal protein L39 [AAX43773; synthetic construct]	51 (100%)	1E-22	Unknown	2.976	0.289
CB493489	Ribosomal protein L41 [AB374982; *Solea senegalensis*] [(N)] (*Oncorhynchus mykiss* type 1)	44 (100%)	3E-12	Structural constituent of ribosome (GO:0003735) [A9ZTC2]	2.871	0.674
CK991221	Ribosomal protein L41 [AB374982; *Solea senegalensis*] [(N)] (*Oncorhynchus mykiss* type 2)	85 (93%)	4E-25	Structural constituent of ribosome (GO:0003735) [A9ZTC2]	2.391	0.495
CB510505	Ribosomal protein S30 [ACA05173; *Oncorhynchus*	133 (100%)	2E-58	Structural constituent of ribosome	1.954	0.165

	masou formosanus]			(GO:0003735) [B1A311]		
CA038670	RNase 2 [ABY55257; *Oncorhynchus masou formosanus*] (*Salmo salar* feature)	141 (71%)	3E-51	Nucleic acid binding; Pancreatic ribonuclease activity (GO:0003676; GO:0004522) [B0FFJ3]	2.630	0.511
CB510556	RNase 2 [ABY55257; *Oncorhynchus masou formosanus*] (*Salmo salar* feature)	141 (71%)	3E-51	Nucleic acid binding; Pancreatic ribonuclease activity (GO:0003676; GO:0004522) [B0FFJ3]	2.521	0.328
CA037923	RWD domain-containing protein 1 [ACO07902; *Oncorhynchus mykiss*]	117 (100%)	6E-59	Unknown	24.086	19.139
CB507020	S100 calcium binding protein [CAJ90906; *Salmo salar*]	141 (88%)	4E-58	Calcium ion binding (GO:0005509) [Q0KFS2]	2.578	0.289
DW569816	Salivary secreted glycine rich protein [ABR23496; *Ornithodoros parkeri*]	142 (31%)	3E-10	Unknown	8.796	3.573
CA037380	Secreted phosphoprotein 24 [CAD21625; *Salmo salar*]	79 (100%)	2E-33	Extracellular region (GO:0005576) [Q710A1] [c]	2.234	0.365
CA049981	Selenoprotein Pa precursor [BT072221; *Salmo salar*] [(N)] (*Salmo salar* type 2) (SEPP2, Fig. 15B)	583 (99%)	0	Unknown	2.376	0.342
CB498862	Selenoprotein Pa precursor [BT072221; *Salmo salar*] [(N)] (*Salmo salar* type 2) (SEPP2, Fig. 15B)	696 (99%)	0	Unknown	2.572	0.314
CA769454	Selenoprotein Pa precursor [BT072678; *Salmo salar*] [(N)] (*Salmo salar* type 1) (SEPP1, Fig. 15A)	706 (100%)	0	Unknown	12.663	4.341
CA044863	Selenoprotein S [ACN10331;	60 (100%)	5E-27	Selenium binding (GO:0008430)	3.807	0.447

	Salmo salar]			[C0H8G2]		
CA038637	Serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1 [CAQ14779; *Danio rerio*]	32 (88%)	3E-9	Serine-type endopeptidase inhibitor activity (GO:0004867) [B0V3R7]	5.328	1.965
CA052126	Serine incorporator 1 [BT045730; *Salmo salar*] (N)	670 (99%)	0	Membrane (GO:0016020) [B5X3W1] [c]	6.008	3.354
CB494451	Serum albumin [ABF57673; *Oncorhynchus mykiss*]	165 (99%)	4E-84	Extracellular space (GO:0005615) [A5H0J9] [c]	4.108	0.997
CA037647	Serum albumin 2 [CAA43187; *Salmo salar*] (*Salmo salar* type 1)	130 (99%)	2E-62	Lipid binding; Metal ion binding (GO:0008289; GO:0046872) [Q03156]	6.208	2.111
EG910863	Serum albumin 2 [CAA43187; *Salmo salar*] (*Salmo salar* type 2)	232 (78%)	1E-96	Lipid binding; Metal ion binding (GO:0008289; GO:0046872) [Q03156]	5.714	0.925
CB509749	Serum amyloid P component precursor [AAA40093; *Mus musculus*] (X)	108 (47%)	8E-22	Metal ion binding; Sugar binding (GO:0046872; GO:0005529) [P12246]	4.264	1.360
CB498256	Similar to non-LTR retrotransposable element [AAP06232; *Schistosoma japonicum*]	125 (47%)	8E-13	RNA binding; RNA-directed DNA polymerase activity (GO:0003723; GO:0003964) [Q86EK6]	2.842	0.477
CB510373	Small EDRK-rich factor 2 [ACM08444; *Salmo salar*]	61 (100%)	8E-27	Unknown	5.035	1.608
CA049970	Small nuclear ribonucleoprotein Sm D2 [BT125385; *Salmo salar*] (N)	656 (100%)	0	Nucleic acid binding (GO:0003676) [B5XGC3]	4.573	2.397
CB499976	Southpaw [BAF35855; *Paralichthys olivaceus*]	45 (85%)	8E-17	Growth factor activity (GO:0008083) [A0A7V0]	2.302	0.250
CB492428	SPARC precursor [ACI34168; *Salmo salar*] (*Oncorhynchus*	55 (84%)	5E-25	Calcium ion binding (GO:0005509) [B5X4D7]	4.866	0.954

	mykiss feature)					
CA048079	SPARC precursor [BT045906; *Salmo salar*] [(N)] (*Salmo salar* feature)	499 (99%)	0	Calcium ion binding (GO:0005509) [B5X4D7]	29.234	19.208
CA352182	Splicing factor, arginine/serine-rich 1 [BT059149; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* feature)	530 (95%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [C0H9Z3]	10.021	3.720
CB516484	Splicing factor, arginine/serine-rich 6 [BT045549; *Salmo salar*] [(N)] (*Salmo salar* feature)	650 (99%)	0	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [B5X3D0]	2.633	0.603
CB517593	Sprouty homolog 2 [BC095266; *Danio rerio*] [(N)(X)]	755 (97%)	0	Membrane (GO:0016020) [Q4VBS7] [c]	4.308	2.396
CA043364	Sterol carrier protein 2 [AAH63230; *Danio rerio*]/[EZ771593; *Oncorhynchus mykiss*] [(B)]	149 (72%)/ 498 (91%)	5E-52/ 0	Sterol binding; Transferase activity, transferring acyl groups other than amino-acyl groups (GO:0032934; GO:0016747) [Q6P4V5]	3.413	1.142
CB512613	Stress-associated endoplasmic reticulum protein family member 2 [AAI00484; *Mus musculus*] [(X)]	53 (85%)	2E-17	Endoplasmic reticulum membrane; Integral to membrane (GO:0005789; GO:0016021) [Q6TAW2] [c]	3.141	1.342
CB493904	Tc1-like transporase [BAF37936; *Oncorhynchus mykiss*]	214 (96%)	4E-119	DNA binding; Transposase activity (GO:0003677; GO:0004803) [A0P9K9]	2.628	0.607
CB493026	Thioredoxin [ACM09596; *Salmo salar*]	110 (81%)	2E-41	Cell redox homeostasis (GO:0045454) [B9EPZ9] [b]	2.727	0.828
CB494082	Thioredoxin-interacting protein [BT058954; *Salmo salar*] [(N)]	242 (92%)	5E-85	Unknown	2.605	0.487
CA060861	Thumpd2-prov protein [AAH77569; *Xenopus laevis*]	85 (43%)	4E-6	Unknown	3.051	1.084
CA064059	Thymosin beta-11 [BT057462; *Salmo salar*] [(N)] (*Salmo salar* feature)	672 (99%)	0	Actin binding (GO:0003779) [B5XB79]	6.357	3.248

CB496527	Thymosin beta-11 [BT125210; *Salmo salar*] [(N)] (*Oncorhynchus mykiss* feature)	676 (94%)	0	Actin binding (GO:0003779) [B5XB79]	2.246	0.394
CB493750	Thymosin beta-12 [ACI67890; *Salmo salar*] (*Oncorhynchus mykiss* feature)	43 (94%)	3E-14	Actin binding (GO:0003779) [B5XAM0]	5.271	2.031
CB506047	Thymosin beta-12 [ACI67890; *Salmo salar*] (*Salmo salar* feature)	43 (100%)	4E-8	Actin binding (GO:0003779) [B5XAM0]	3.751	1.066
CB509551	Thymosin beta-12 [ACI67890; *Salmo salar*] (*Salmo salar* feature)	43 (100%)	2E-8	Actin binding (GO:0003779) [B5XAM0]	3.374	0.873
CA038301	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*] (*Salmo salar* type 1)	76 (90%)	5E-30	Unknown	8.453	1.614
CA769178	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*] (*Salmo salar* type 2)	76 (90%)	2E-30	Unknown	5.437	1.757
CA051958	Trafficking protein particle complex subunit 3 [BT060107; *Salmo salar*] [(N)]	711 (99%)	0	Guanylate cyclase activity; Heme binding (GO:0004383; GO:0020037) [C0H7U8]	2.499	0.528
CB496771	Transferrin [BAA84103; *Oncorhynchus mykiss*]	89 (100%)	8E-44	Ferric iron binding (GO:0008199) [Q9PT13]	10.042	3.088
CA060894	Transketolase-like protein 2 [BT072448; *Salmo salar*] [(N)]	657 (98%)	0	Catalytic activity (GO:0003824) [C0PUI7]	2.654	0.493
CB516126	Translocon-associated protein subunit delta precursor [BT057917; *Salmo salar*] [(N)]	701 (100%)	0	Endoplasmic reticulum; Integral to membrane (GO:0005783; GO:0016021) [B9EQJ2] [c]	2.665	0.674
CA056207	Transmembrane protein 179B [ACM08784; *Salmo salar*]	44 (100%)	6E-8	Integral to membrane (GO:0016021) [B9EMN7] [c]	3.576	1.522
CA043526	Transposable element Tc1	147 (80%)	6E-49	DNA binding; Transposase activity	4.610	1.999

	transposase [ACI68988; *Salmo salar*]			(GO:0003677; GO:0004803) [B5XDR8]		
CB510698	Transposable element Tcb1 transposase [BT072386; *Salmo salar*] (N) (*Salmo salar* type 2)	120 (93%)	3E-38	Unknown	9.002	4.211
CA048856	Transposable element Tcb2 transposase [ACN10944; *Salmo salar*]	52 (89%)	2E-30	Unknown	8.158	1.813
CB509934	Transposase [BAA83461; *Oryzias latipes*] (*Salmo salar* type 3)	44 (66%)	5E-9	Nucleic acid binding (GO:0003676) [Q9PTV0]	15.770	12.878
CA047299	Transposase-like mRNA [BT043992; *Salmo salar*] (N)	339 (80%)	1E-50	DNA binding; Transposase activity (GO:0003677; GO:0004803) [B5RI68]	4.199	0.705
CA048447	Tripartite motif-containing protein 16 [BT045784; *Salmo salar*] (N) (*Salmo salar* feature)	623 (99%)	0	Zinc ion binding (GO:0008270) [B5X415]	3.583	0.559
CA050082	Tripartite motif-containing protein 16 [BT045784; *Salmo salar*] (N) (*Salmo salar* feature)	640 (99%)	0	Zinc ion binding (GO:0008270) [B5X415]	3.462	0.648
CB498971	Tripartite motif-containing protein 16 [BT045784; *Salmo salar*] (N) (*Salmo salar* feature)	715 (99%)	0	Zinc ion binding (GO:0008270) [B5X415]	2.830	0.635
CB499762	Tripartite motif-containing protein 16 [BT045784; *Salmo salar*] (N) (*Salmo salar* feature)	685 (97%)	0	Zinc ion binding (GO:0008270) [B5X415]	2.490	0.264
CX245969	Tryptophan 2,3-dioxygenase [AAI51921; *Danio rerio*]	238 (83%)	2E-103	Iron ion binding; Tryptophan 2,3-dioxygenase activity (GO:0005506; GO:0004833) [A7MBU6]	3.633	0.548
CA058349	Tubulin, delta 1 [AAH71532; *Danio rerio*]	101 (74%)	2E-37	GTP binding; GTPase activity; Structural molecule activity (GO:0005525; GO:0003924; GO:0005198) [Q6IQ78]	2.946	0.545
CB498518	Type I collagen alpha 2 chain	191	3E-34	Extracellular matrix structural constituent	2.494	0.540

	[BAB79230; *Oncorhynchus keta*]	(100%)		(GO:0005201) [Q8UUJ3]		
CA054066	Ubiquitin [ACN10141; *Salmo salar*]	156 (100%)	5E-82	Unknown	3.520	1.263
EG816865	Ubiquitin-conjugating enzyme E2 D2 [BT045193; *Salmo salar*] (N)	242 (100%)	2E-122	Small conjugating protein ligase activity (GO:0019787) [B5X1W6]	4.116	1.751
DY704284	Ubiquitin-conjugating enzyme E2 variant 3 [BT045603; *Salmo salar*] (N)	520 (91%)	0	Binding; Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; Small conjugating protein ligase activity (GO:0005488; GO:0016616; GO:0019787) [B5X3I4]	3.973	1.506
CA767659	Ubiquitin/ribosomal fusion protein homologue [CAJ90900; *Salmo salar*]	126 (100%)	7E-68	Structural constituent of ribosome (GO:0003735) [Q0KFS8]	3.183	0.770
CB497940	UDP glucuronosyltransferase 1 family polypeptide a3 isoform 1 [ADC91921; *Danio rerio*]	231 (74%)	8E-101	Transferase activity, transferring hexosyl groups (GO:0016758) [D3XD50]	2.157	0.294
CA037110	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.499	0.314
CA037849	Unknown (no significant BLAST hits)	NA	NA	Unknown	7.023	1.646
CA043133	Unknown (no significant BLAST hits)	NA	NA	Unknown	4.117	0.829
CA044555	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.389	0.247
CA044829	Unknown (no significant BLAST hits)	NA	NA	Unknown	33.335	19.590
CB514412	Unknown (no significant BLAST hits)	NA	NA	Unknown	4.012	1.828
CA052592	Unknown (no significant BLAST	NA	NA	Unknown	3.094	0.797

	hits)					
CA053884	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.441	1.002
CA056776	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.239	0.287
CA059408	Unknown (no significant BLAST hits)	NA	NA	Unknown	4.200	1.600
CA345164	Unknown (no significant BLAST hits)	NA	NA	Unknown	9.479	3.686
CA368985	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.359	1.230
CA374889	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.358	1.355
CA770673	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.723	0.784
CB492559	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.052	0.296
CB494674	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.002	0.307
CB498122	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.017	0.647
CB502713	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.811	0.428
CB509762	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.391	0.792
CB510700	Unknown (no significant BLAST hits)	NA	NA	Unknown	30.090	15.646
CK990274	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.454	0.201

CK991349	Unknown (no significant BLAST hits)	NA	NA	Unknown	11.537	4.986
DW544537	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.527	0.476
DW567009	Unknown (no significant BLAST hits)	NA	NA	Unknown	10.191	5.390
DY737345	Unknown (no significant BLAST hits)	NA	NA	Unknown	4.268	1.834
EG804144	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.702	0.400
EG805608	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.722	0.611
EG837877	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.437	0.168
EG863678	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.662	0.361
EG902586	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.314	0.241
FC072802	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.602	1.455
CA055287	Uroporphyrinogen decarboxylase [ACI33757; *Salmo salar*]	55 (99%)	9E-23	Uroporphyrinogen decarboxylase activity (GO:0004853) [B5X376]	3.155	0.654
CA050997	V-Fos transformation effector (ribosomal protein S3A) [ACH70890; *Salmo salar*]	236 (100%)	3E-132	Structural constituent of ribosome (GO:0003735) [B5DGL6]	2.339	0.357
DW540022	Vitamin D receptor a [AAI62213; *Danio rerio*]	216 (90%)	8E-87	Sequence-specific DNA binding; Sequence-specific DNA binding transcription factor activity; Steroid hormone receptor activity; Transcription regulator activity; Vitamin D binding; Zinc ion binding (GO:0043565;	2.857	0.060

				GO:0003700; GO:0003707; GO:0030528; GO:0005499; GO:0008270) [Q9PTN2]		
DW552997	Widely-interspaced zinc finger motifs (predicted) [EDL89467; *Rattus norvegicus*]/[DW545274; *Salmo salar*] (B)	209 (42%)	2E-24	Zinc ion binding (GO:0008270) [D3ZQQ2]	1.989	0.203
CB503106	Y-box binding protein [ACL31579; *Oncorhynchus mykiss*]	71 (100%)	2E-21	DNA binding (GO:0003677) [B8Y7S9]	3.067	0.518
CK990349	Y-box binding protein [BT043918; *Salmo salar*] (N)	340 (98%)	2E-159	DNA binding (GO:0003677) [B5DH09]	2.555	0.187
DW566726	Zinc finger, FYVE domain containing 9 [CAO77959; *Mus musculus*]	202 (69%)	1E-69	Protein binding; Zinc ion binding (GO:0005515; GO:0008270) [A8Y5G5]	2.663	0.598
CA044097	Zinc transporter ZIP1 [BT057412; *Salmo salar*] (N)	620 (100%)	0	Metal ion transmembrane transporter activity (GO:0046873) [B9EP37]	26.266	13.518
CA054221	Zonadhesin-like gene [AY785950; *Salmo salar*] (N)	448 (85%)	3E-110	Membrane (GO:0016020) [Q5S3N1] c	2.298	0.287

Please see Appendix II for footnotes.

APPENDIX V. Supplemental table containing 102 transcripts with greater than 2-fold higher expression in triploid growth hormone transgenic (3NGHTg) Atlantic salmon family AS25 (slow-growing) in comparison to 3NGHTg Atlantic salmon family AS26 (fast-growing) in any 3 out of 4 technical replicate microarrays including at least one dye-swap.

EST	Gene Name of Best BLASTX or BLASTN [(N)] Hit	Length (% ID)	E value	Function of Best BLAST Hit	$\overline{X}$ Fold Change	SE
CA053974	6-Phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 [ACI34300; *Salmo salar*]	116 (100%)	7E-62	6-Phosphofructo-2-kinase activity; ATP binding (GO:0003873; GO:0005524) [B5X4R9]	3.006	0.673
CA063003	Acyl-CoA dehydrogenase family member 10 [BT045545; *Salmo salar*] [(N)]	628 (100%)	0	Hydrolase activity (GO:0016787) [B5X3C6]	3.525	1.162
CK990279	ADAMTS-1 protein [BAE16358; *Oryzias latipes*] (ADAMTS1, Fig. 11F)	148 (72%)	1E-58	Metalloendopeptidase activity; Zinc ion binding (GO:0004222; GO:0008270) [Q4AED3]	12.319	8.837
CA050985	Adaptor related protein complex (AP)-3 delta subunit [BAA36591; *Bos taurus*] [(G)]	1203 (72%)	4E-70	Binding; Protein transporter activity (GO:0005488; GO:0008565) [Q865S1]	5.712	1.421
EG918344	Alpha-tubulin [AAA68904; *Oncorhynchus mykiss gairdneri*]	240 (99%)	8E-138	GTP binding; GTPase activity; Structural molecule activity (GO:0005525;GO:0003924; GO:0005198) [P18288]	2.153	0.128
CA062526	Apelin receptor B [BT058745; *Salmo salar*] [(N)]	594 (99%)	0	Purinergic nucleotide receptor activity, G-protein coupled (GO:0045028) [C0H8T9]	3.137	0.842
CA051980	ATP synthase subunit alpha, mitochondrial precursor	125 (99%)	1E-61	ATP binding; Hydrogen ion transporting ATP synthase activity, rotational	4.404	0.852

	[ACI33076; *Salmo salar*]			mechanism; Proton-transporting ATPase activity, rotational mechanism (GO:0005524; GO:0046933; GO:0046961) [B5X195]		
CB518061	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c-3 [ACH70907; *Salmo salar*]	139 (100%)	5E-57	Hydrogen ion transporting ATP synthase activity, rotational mechanism (GO:0046933) [B5DGN3]	6.908	2.607
CA047841	Cellular nucleic acid-binding [BT056750; *Salmo salar*] (N)	672 (99%)	0	Nucleic acid binding; Zinc ion binding (GO:0003676; GO:0008270) [B9EM75]	7.139	3.695
DY735182	Chemokine receptor type 3 [BT059440; *Salmo salar*] (N)	117 (84%)	3E-18	C-C chemokine receptor activity (GO:0016493) [C0HAT4]	5.522	3.034
CA043676	Cisplatin resistance-associated overexpressed protein [BT059502; *Salmo salar*] (N)	582 (99%)	0	Unknown	7.221	4.571
EG849106	Claudin 28b [ACK86563; *Oncorhynchus mykiss*]	175 (99%)	4E-68	Structural molecule activity (GO:0005198) [C7S8F2]	5.375	2.205
DW546950	Claudin-3 [BT044690; *Salmo salar*] (N)	782 (99%)	0	Structural molecule activity (GO:0005198) [B5X0X1]	16.523	9.856
CA058146	Complement factor D precursor [ACI69539; *Salmo salar*]	193 (99%)	1E-109	Serine-type endopeptidase activity (GO:0004252) [B5XFB9]	2.562	0.414
DY736164	Death-inducer obliterator 1 [CBN81033; *Dicentrarchus labrax*]	273 (53%)	9E-55	Unknown	3.939	0.967
EG866333	DOM-3 homolog Z [EDL83433; *Rattus norvegicus*]/[v; *Oncorhynchus nerka*] (B)	62 (65%)/ 210 (93%)	4E-19/ 3e-78	Unknown	5.193	2.200
DY696111	Dynactin subunit 5 [ACM08710; Salmo salar]	169 (99%)	6E-84	Transferase activity (GO:0016740) [B9EMG3]	2.698	0.468
EG876950	Ectonucleotide pyrophosphatase/phosphodiester	477 (85%)	7E-124	Hydrolase activity; Metal ion binding; Nucleic acid binding (GO:0016787;	4.498	1.906

	ase family member 2 precursor [BT072143; *Salmo salar*] (N)			GO:0046872; GO:0003676) [C0PU84]		
CB504468	Elastase 2-like protein [AAT45251; *Sparus aurata*]	180 (78%)	6E-70	Serine-type endopeptidase activity (GO:0004252) [Q4QY81]	4.740	0.919
EG758627	Elongation factor, RNA polymerase II, 2 [BT049474; *Salmo salar*] (N)	70 (85%)	9E-8	RNA polymerase II transcription elongation factor activity; Translation elongation factor activity (GO:0016944; GO:0003746) [B5XEK5]	2.177	0.087
CA059829	Eukaryotic translation initiation factor 3 subunit 3 [ACO08262; *Oncorhynchus mykiss*]	106 (99%)	2E-45	Translation initiation factor activity (GO:0003743) [C1BGV9]	3.066	0.695
CB515458	Ezrin-radixin-moesin-binding phosphoprotein 50 [BT045262; *Salmo salar*] (N)	802 (98%)	0	Unknown	2.683	0.508
CK991289	Fast myotomal muscle tropomyosin [AAB36559; *Salmo salar*]/[EZ908341; *Oncorhynchus mykiss*] (B)	237 (99%)/ 386 (96%)	7E-121/ 2e-173	Unknown	3.113	1.136
DW562013	Growth hormone 2 [EU621899; *Salmo salar*] (N)	86 (85%)	1E-11	Hormone activity (GO:0005179) [B2Z9Z2]	3.544	1.155
CB501529	Guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2a [AAH59612; *Danio rerio*]	44 (71%)	0.0000 00004	Signal transducer activity (GO:0004871) [Q6PBR4]	4.744	2.024
CA051350	Interferon-induced protein with tetratricopeptide repeats 5 [ACI34283; *Salmo salar*]	141 (100%)	2E-75	Binding (GO:0005488) [B5X4Q2]	2.688	0.331
CX248319	Interferon-inducible GTPase_b and interferon-inducible GTPase_a [EU221179; *Salmo salar*] (N)	49 (94%)	5E-10	GTP binding; Hydrolase activity, acting on acid anhydrides (GO:0005525; GO:0016817) [A8WCJ8]	2.108	0.424
EG887324	Leukocyte elastase inhibitor	70 (95%)	3E-19	Serine-type endopeptidase inhibitor	11.229	3.988

	[BT044977; *Salmo salar*] [(N)]			activity (GO:0004867) [B5X1Q8]		
DY728189	Membrane-spanning transport protein 1 [AAK58462; *Mus musculus*] [(X)]	209 (73%)	3E-86	Developmental pigmentation; Transmembrane transport (GO:0048066; GO:0055085) [Q541S3] [b]	10.255	4.528
CB490715	MHC class I b region [AB162343; *Oncorhynchus mykiss*] [(N)]	329 (95%)	3E-142	MHC class I protein complex (GO:0042612) [Q5FBT8] [c]	2.762	0.830
DW557989	MHC class II antigen beta chain [EU008541; *Salmo salar*] [(N)]	69 (92%)	2E-15	MHC class II protein complex; integral to membrane (GO:0042613; GO:0016021) [B2XBN8] [c]	3.817	1.263
DY715252	Microtubule associated serine/threonine kinase-like [AAH78324; *Danio rerio*] [(X)]	169 (73%)	2E-49	ATP binding; Protein serine/threonine kinase activity (GO:0005524; GO:0004674) [Q6DBX4]	3.911	1.238
CX025770	Myotilin [AAD44754|AF144477; *Homo sapiens*] [(X)]	151 (51%)	1E-40	Actin binding; Structural constituent of muscle (GO:0003779; GO:0008307) [Q9UBF9]	6.699	1.848
CA043373	N-acetylated alpha-linked acidic dipeptidase-like 1 [AAI71342; *Danio rerio*]	62 (68%)	1E-14	Peptidase activity (GO:0008233) [A2BGQ8]	1.895	0.271
CA057355	N-acylneuraminate cytidylyltransferase [BT044895; *Salmo salar*] [(N)]	297 (97%)	1E-136	Nucleotidyltransferase activity (GO:0016779) [B5X1H6]	5.467	2.978
CA051243	NEDD8-activating enzyme E1 catalytic subunit [ACI33010; *Salmo salar*]	105 (100%)	5E-51	ATP binding; Acid-amino acid ligase activity; Small protein activating enzyme activity (GO:0005524; GO:0016881; GO:0008641) [B5X129]	2.101	0.381
DW575702	NOD-like receptor C [ABU89560; *Danio rerio*]/[EZ780618; *Oncorhynchus mykiss*] [(B)]	152 (45%)/ 172 (92%)	6E-22/ 1E-56	Receptor activity (GO:0004872) [A8DY17]	6.272	2.414
CA048081	Non-histone chromosomal protein	549 (99%)	0	DNA binding (GO:0003677) [B9ELY5]	2.074	0.090

	H6 [BT057525; *Salmo salar*] [N]					
CX245387	Novel major facilitator superfamily protein [CAL49372; *Xenopus (Silurana) tropicalis*]	108 (36%)	4E-12	Transmembrane transport (GO:0055085) [Q07G00] [b]	6.747	2.745
CX248767	Novel protein similar to vertebrate exosome component 1 [CAX13911; *Danio rerio*]/[EZ777662; *Oncorhynchus mykiss*] [B]	124 (83%)/ 701 (99%)	9E-48/ 0	Nucleolus (GO:0005730) [B8A4H5]	3.299	1.098
CA061927	Novel protein similar to vertebrate pogo transposable element with ZNF domain (POGZ) [CAP09536; *Danio rerio*]	156 (41%)	3E-22	Nucleic acid binding; Zinc ion binding (GO:0003676; GO:0008270) [A8E7N7]	3.363	0.917
DY738218	Nuclear VCP-like [AAH44464; *Danio rerio*]	78 (66%)	1E-15	ATP binding; Nucleoside-triphosphatase activity (GO:0005524; GO:0017111) [Q803I9]	4.521	1.924
DW550792	ORM1-like 3 (S. cerevisiae) [AAH46594; *Mus musculus*] [X]	109 (89%)	5E-44	SPOTS complex; Integral to membrane (GO:0035339; GO:0016021) [Q9CPZ6] [c]	2.523	0.625
CA061377	Ornithine decarboxylase 1 [BT045263; *Salmo salar*] [N]	721 (99%)	0	Ornithine decarboxylase activity (GO:0004586) [B5X2J4]	3.028	0.529
CA063676	Ortholog of mouse zinc finger protein ZFP64 [CAB90277; *Homo sapiens*] [G]	627 (43%)	4.6E-37	DNA binding; Zinc ion binding (GO:0003677; GO:0008270) [Q9NPA5]	2.913	0.750
CB499376	Peptidyl-prolyl cis-trans isomerase A [ACM09531; *Salmo salar*]	164 (99%)	8E-85	Peptidyl-prolyl cis-trans isomerase activity (GO:0003755) [B9EPT4]	2.382	0.522
EG924333	Polyunsaturated fatty acid elongase gene [GU238431; *Salmo salar*] [N]	101 (94%)	4E-32	Integral to membrane (GO:0016021) [Q8AWE7] [c]	6.872	3.138
CA051811	Probable dimethyladenosine transferase [ACI69951; *Salmo*	150 (100%)	1E-80	rRNA (adenine-N6,N6-)-dimethyltransferase activity	4.011	0.589

	salar]			(GO:0000179) [B5XGI1]		
DW547065	Protein-glutamine gamma-glutamyltransferase K [BT045232; *Salmo salar*] [(N)]	65 (100%)	7E-24	Protein-glutamine gamma-glutamyltransferase activity (GO:0003810) [B5X2G3]	3.582	1.256
CA057207	Pyruvate kinase [BT043851; *Salmo salar*] [(N)]	642 (99%)	0	Magnesium ion binding; Potassium ion binding; Pyruvate kinase activity (GO:0000287; GO:0030955; GO:0004743) [B5DGU1]	3.327	1.024
CB511710	Serine/threonine-protein kinase 6 [ACI33637; *Salmo salar*]	185 (100%)	8E-106	ATP binding; Protein serine/threonine kinase activity (GO:0005524; GO:0004674) [B5X2V6]	2.658	0.598
CA055683	Serine/threonine-protein phosphatase 6[BT071995; *Salmo salar*] [(N)]	570 (99%)	0	Phosphoprotein phosphatase activity (GO:0004721) [C0PU36]	9.343	6.098
CB514742	Sideroflexin-1 [ADO27796; *Ictalurus furcatus*]	107 (87%)	2E-45	Cation transmembrane transporter activity (GO:0008324) [E3TBW0]	5.440	2.452
CB517023	Small glutamine-rich tetratricopeptide repeat (TPR)-containing mRNA [BT043722; *Salmo salar*] [(N)]	715 (99%)	0	Binding (GO:0005488) [B5DGG3]	7.047	3.268
CB510411	Small heat shock protein [ACO56893; *Epinephelus coioides*]	193 (94%)	2E-100	Response to stress (GO:0006950) [C1KGR5] [b]	3.668	0.997
CB503927	SPRY domain-containing protein 4 [ACI66729; *Salmo salar*]	205 (100%)	8E-116	Unknown	2.556	0.395
EG888926	Structural maintenance of chromosomes 1B [CAQ08672; *Homo sapiens*]	40 (75%)	6E-10	ATP binding (GO:0005524) [Q8NDV3]	2.616	0.476
CA062748	Suppressor of IKK-epsilon [BT045625; *Salmo salar*] [(N)]	82 (92%)	4E-21	Unknown	2.285	0.249
CA052912	TATA box binding protein	450 (52%)	4E-27	DNA binding; RNA polymerase I	3.075	1.355

	(TBP)-associated factor, RNA polymerase I, A, 48kD [AAH13808; *Homo sapiens*] [(G)]			transcription factor activity; General RNA polymerase II transcription factor activity (GO:0003677; GO:0003701; GO:0016251) [Q15573]		
CA043704	Tetratricopeptide repeat protein 32 [ACI67454; *Salmo salar*]	38 (100%)	1E-13	Binding (GO:0005488) [B5X9D4]	3.131	0.609
BX080010	TNF receptor-associated factor 6 [BAI68387; *Plecoglossus altivelis altivelis*]	255 (68%)	3E-93	Receptor activity; Ubiquitin-protein ligase activity; Zinc ion binding (GO:0004872; GO:0004842; GO:0008270) [D2Z011]	3.482	0.892
CA056951	Transmembrane protein 50A [BT125442; *Salmo salar*] [(N)]	728 (99%)	0	Integral to membrane (GO:0016021) [B5XE68] [c]	2.564	0.579
DY727127	Transport-associated protein Tap2A [Z83328; *Salmo salar*] [(N)]	381 (94%)	7E-158	ATP binding; ATPase activity, coupled to transmembrane movement of substances (GO:0005524; GO:0042626) [P79909]	2.745	0.593
FC072841	Transposable element Tcb1 transposase [ACN11475; *Salmo salar*]	88 (56%)	9E-15	DNA binding; Transposase activity (GO:0003677; GO:0004803) [C0HBQ6]	2.766	0.561
CA063300	Tripartite motif-containing protein 35 [ACO09553; *Osmerus mordax*]	119 (40%)	6E-21	Zinc ion binding (GO:0008270) [C1BKK0]	6.995	2.940
EG815176	TSR1 protein [AAI61761; *Xenopus (Silurana) tropicalis*]	174 (74%)	3E-74	Nucleus (GO:0005634) [B1WBH9] [b]	2.429	0.514
CA050457	TSR1, 20S rRNA accumulation, homolog (yeast) [CAI24249; *Mus musculus*]	174 (71%)	2E-71	Nucleus (GO:0005634) [Q5SWD9] [b]	2.475	0.464
DW562672	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.019	0.744
CA055445	Unknown (no significant BLAST hits)	NA	NA	Unknown	11.292	5.382
DW551703	Unknown (no significant BLAST hits)	NA	NA	Unknown	8.118	3.725

CX027104	Unknown (no significant BLAST hits)	NA	NA	Unknown	7.751	4.577
DW536234	Unknown (no significant BLAST hits)	NA	NA	Unknown	7.239	5.062
CA045970	Unknown (no significant BLAST hits)	NA	NA	Unknown	7.219	4.700
DW536177	Unknown (no significant BLAST hits)	NA	NA	Unknown	6.310	3.086
CX136687	Unknown (no significant BLAST hits)	NA	NA	Unknown	5.793	2.812
DW555961	Unknown (no significant BLAST hits)	NA	NA	Unknown	5.695	3.043
EG793806	Unknown (no significant BLAST hits)	NA	NA	Unknown	4.898	1.476
CA036909	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.411	0.938
CA051106	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.387	0.763
DW533540	Unknown (no significant BLAST hits)	NA	NA	Unknown	3.066	0.468
CA060174	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.968	0.930
EG942110	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.833	0.379
CA044652	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.799	0.338
DW575806	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.709	0.381
CA057380	Unknown (no significant BLAST	NA	NA	Unknown	2.570	0.725

	hits)					
CA051846	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.514	0.475
EG812600	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.480	0.491
DW560079	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.389	0.586
CB516735	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.385	0.532
DW554684	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.360	0.518
CA052657	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.350	0.500
CB517198	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.123	0.313
DY708685	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.102	0.311
DW581026	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.084	0.218
DW581367	Unknown (no significant BLAST hits)	NA	NA	Unknown	2.044	0.214
DW570466	V-set and transmembrane domain-containing protein 2-like protein precursor [BT072624; *Salmo salar*] [(N)]	681 (100%)	0	Unknown	5.649	3.177
CK990233	WD repeat domain containing 82 [AAH31502; *Mus musculus*] [(X)]	68 (92%)	6E-32	PTW/PP1 phosphatase complex; Chromatin (GO:0072357; GO:0000785) [Q8BFQ4] [c]	2.374	0.195
CA062063	WD repeat-containing protein 68 [BT045482; *Salmo salar*] [(N)]	195 (79%)	4E-21	Unknown	2.143	0.328

CX042505	Widely interspaced zinc finger motifs [AAI44333; *Homo sapiens*]	224 (34%)	4E-25	Zinc ion binding (GO:0008270) [B7ZM82]	2.319	0.433
EG886818	Zinc finger protein 572 [ACI69402; *Salmo salar*]	233 (34%)	5E-12	Nucleic acid binding; Zinc ion binding (GO:0003676; GO:0008270) [B5XEY2]	2.732	0.626
CA059714	Zinc finger protein 748 [AAH55310; *Mus musculus*]	54 (45%)	3E-8	Nucleic acid binding; Zinc ion binding (GO:0003676; GO:0008270) [Q7TPL6]	2.065	0.273
CA047891	Zymogen granule membrane protein 16 precursor [BT057902; *Salmo salar*] (N)	655 (99%)	0	Unknown	2.805	0.529

Please see Appendix II for footnotes.

APPENDIX VI. Supplemental tables showing QPCR relative quantity (RQ) data for informative transcripts normalized to PABP1 mRNA expression.

Appendix VI. A. QPCR relative quantity (RQ) data for ACBP normalized to PABP1 mRNA expression

Sample name	RQ	Average	SE	Fold change AS11/AS25	Fold change AS26/AS25
AS11_3N_151_F	4.10	6.19	0.93	1.39	1.67
AS11_3N_155_F	9.52				
AS11_3N_156_M	3.57				
AS11_3N_160_F	5.27				
AS11_3N_161_M	6.11				
AS11_3N_162_F	5.14				
AS11_3N_166_M	9.64				
AS25_3N_154_F	7.89	4.46	0.66		
AS25_3N_155_F	6.03				
AS25_3N_156_M	3.00				
AS25_3N_157_M	3.06				
AS25_3N_159_F	2.46				
AS25_3N_160_M	5.37				
AS25_3N_164_F	3.33				
AS25_3N_167_F	4.52				
AS26_3N_253_F	2.24	7.44	2.39		
AS26_3N_254_F	21.83				
AS26_3N_256_M	5.97				
AS26_3N_257_F	12.15				
AS26_3N_260_M	6.69				
AS26_3N_261_F	6.61				
AS26_3N_263_M	1.00				
AS26_3N_265_F	3.05				

Appendix VI. B. QPCR relative quantity (RQ) data for APOAIV normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	6.92	32.39	10.83	3.71	5.08
AS11_3N_155_F	84.03				
AS11_3N_156_M	29.07				
AS11_3N_160_F	6.84				
AS11_3N_161_M	49.87				
AS11_3N_162_F	41.22				
AS11_3N_166_M	8.76				
AS25_3N_154_F	5.28	8.73	2.75		
AS25_3N_155_F	23.49				
AS25_3N_156_M	6.47				
AS25_3N_157_M	1.00				
AS25_3N_159_F	4.70				
AS25_3N_160_M	3.81				
AS25_3N_164_F	7.01				
AS25_3N_167_F	18.06				
AS26_3N_253_F	36.70	44.36	11.06		
AS26_3N_254_F	92.00				
AS26_3N_256_M	54.17				
AS26_3N_257_F	31.42				
AS26_3N_260_M	16.25				
AS26_3N_261_F	89.27				
AS26_3N_263_M	14.72				
AS26_3N_265_F	20.37				

Appendix VI. C. QPCR relative quantity (RQ) data for APOAI-1 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	1.40	1.76	0.20	1.30	1.97
AS11_3N_155_F	1.85				
AS11_3N_156_M	1.65				
AS11_3N_160_F	1.16				
AS11_3N_161_M	2.75				
AS11_3N_162_F	2.07				
AS11_3N_166_M	1.43				
AS25_3N_154_F	1.48	1.35	0.13		
AS25_3N_155_F	1.32				
AS25_3N_156_M	1.09				
AS25_3N_157_M	2.11				
AS25_3N_159_F	1.17				
AS25_3N_160_M	1.13				
AS25_3N_164_F	1.00				
AS25_3N_167_F	1.50				
AS26_3N_253_F	4.21	2.66	0.27		
AS26_3N_254_F	2.93				
AS26_3N_256_M	2.80				
AS26_3N_257_F	2.39				
AS26_3N_260_M	2.55				
AS26_3N_261_F	2.68				
AS26_3N_263_M	2.18				
AS26_3N_265_F	1.59				

Appendix VI. D. QPCR relative quantity (RQ) data for APOAI-2 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	1.00	3.03	0.53	1.31	2.03
AS11_3N_155_F	4.29				
AS11_3N_156_M	3.59				
AS11_3N_160_F	1.44				
AS11_3N_161_M	4.77				
AS11_3N_162_F	3.50				
AS11_3N_166_M	2.62				
AS25_3N_154_F	2.65	2.32	0.49		
AS25_3N_155_F	3.02				
AS25_3N_156_M	1.57				
AS25_3N_157_M	5.33				
AS25_3N_159_F	1.32				
AS25_3N_160_M	1.24				
AS25_3N_164_F	1.55				
AS25_3N_167_F	1.86				
AS26_3N_253_F	7.92	4.71	0.59		
AS26_3N_254_F	4.99				
AS26_3N_256_M	4.57				
AS26_3N_257_F	4.58				
AS26_3N_260_M	4.33				
AS26_3N_261_F	5.79				
AS26_3N_263_M	2.75				
AS26_3N_265_F	2.74				

Appendix VI. E. QPCR relative quantity (RQ) data for B2M normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	1.82	3.49	0.73	2.20	4.03
AS11_3N_155_F	3.45				
AS11_3N_156_M	3.35				
AS11_3N_160_F	1.68				
AS11_3N_161_M	6.17				
AS11_3N_162_F	6.01				
AS11_3N_166_M	1.92				
AS25_3N_154_F	1.97	1.59	0.14		
AS25_3N_155_F	2.04				
AS25_3N_156_M	1.26				
AS25_3N_157_M	1.83				
AS25_3N_159_F	1.24				
AS25_3N_160_M	1.95				
AS25_3N_164_F	1.38				
AS25_3N_167_F	1.00				
AS26_3N_253_F	5.46	6.39	1.82		
AS26_3N_254_F	4.75				
AS26_3N_256_M	4.88				
AS26_3N_257_F	4.09				
AS26_3N_260_M	7.52				
AS26_3N_261_F	18.56				
AS26_3N_263_M	3.53				
AS26_3N_265_F	2.35				

Appendix VI. F. QPCR relative quantity (RQ) data for B2M2 normalized to PABP1 mRNA expression

Sample name	RQ	Average	SE	Fold change AS11/AS25	Fold change AS26/AS25
AS11_3N_151_F	5.02	16.66	4.34	10.50	8.53
AS11_3N_155_F	17.69				
AS11_3N_156_M	19.55				
AS11_3N_160_F	6.54				
AS11_3N_161_M	39.23				
AS11_3N_162_F	17.69				
AS11_3N_166_M	10.93				
AS25_3N_154_F	1.00	1.59	0.16		
AS25_3N_155_F	1.91				
AS25_3N_156_M	2.45				
AS25_3N_157_M	1.71				
AS25_3N_159_F	1.36				
AS25_3N_160_M	1.60				
AS25_3N_164_F	1.27				
AS25_3N_167_F	1.40				
AS26_3N_253_F	13.91	13.54	3.19		
AS26_3N_254_F	7.67				
AS26_3N_256_M	10.62				
AS26_3N_257_F	13.67				
AS26_3N_260_M	14.57				
AS26_3N_261_F	34.30				
AS26_3N_263_M	8.42				
AS26_3N_265_F	5.17				

Appendix VI. G. QPCR relative quantity (RQ) data for D5DP normalized to PABP1 mRNA expression

Sample name	RQ	Average	SE	Fold change AS11/AS25	Fold change AS26/AS25
AS11_3N_151_F	1.59	6.72	1.78	2.65	5.93
AS11_3N_155_F	8.13				
AS11_3N_156_M	9.39				
AS11_3N_160_F	2.11				
AS11_3N_161_M	14.45				
AS11_3N_162_F	8.37				
AS11_3N_166_M	2.98				
AS25_3N_154_F	2.36	2.53	0.56		
AS25_3N_155_F	4.41				
AS25_3N_156_M	1.00				
AS25_3N_157_M	5.38				
AS25_3N_159_F	1.14				
AS25_3N_160_M	1.90				
AS25_3N_164_F	1.36				
AS25_3N_167_F	2.70				
AS26_3N_253_F	11.50	15.01	3.14		
AS26_3N_254_F	12.56				
AS26_3N_256_M	15.76				
AS26_3N_257_F	13.38				
AS26_3N_260_M	25.08				
AS26_3N_261_F	30.80				
AS26_3N_263_M	5.81				
AS26_3N_265_F	5.22				

Appendix VI. H. QPCR relative quantity (RQ) data for FTM normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	2.51	3.39	0.52	2.08	3.16
AS11_3N_155_F	3.88				
AS11_3N_156_M	4.00				
AS11_3N_160_F	1.80				
AS11_3N_161_M	5.91				
AS11_3N_162_F	3.28				
AS11_3N_166_M	2.36				
AS25_3N_154_F	1.64	1.63	0.16		
AS25_3N_155_F	1.90				
AS25_3N_156_M	1.78				
AS25_3N_157_M	1.00				
AS25_3N_159_F	1.44				
AS25_3N_160_M	2.48				
AS25_3N_164_F	1.45				
AS25_3N_167_F	1.36				
AS26_3N_253_F	4.77	5.15	1.19		
AS26_3N_254_F	3.78				
AS26_3N_256_M	3.45				
AS26_3N_257_F	4.33				
AS26_3N_260_M	9.24				
AS26_3N_261_F	11.39				
AS26_3N_263_M	2.31				
AS26_3N_265_F	1.91				

Appendix VI. I. QPCR relative quantity (RQ) data for GAPDH1 normalized to PABP1 mRNA expression

Sample name	RQ	Average	SE	Fold change AS11/AS25	Fold change AS26/AS25
AS11_3N_151_F	2.90	5.27	1.24	3.23	6.73
AS11_3N_155_F	6.40				
AS11_3N_156_M	6.28				
AS11_3N_160_F	1.02				
AS11_3N_161_M	11.09				
AS11_3N_162_F	5.97				
AS11_3N_166_M	3.25				
AS25_3N_154_F	1.38	1.63	0.22		
AS25_3N_155_F	2.77				
AS25_3N_156_M	1.00				
AS25_3N_157_M	2.36				
AS25_3N_159_F	1.30				
AS25_3N_160_M	1.46				
AS25_3N_164_F	1.02				
AS25_3N_167_F	1.75				
AS26_3N_253_F	8.64	10.98	1.80		
AS26_3N_254_F	12.31				
AS26_3N_256_M	11.58				
AS26_3N_257_F	11.76				
AS26_3N_260_M	15.29				
AS26_3N_261_F	19.30				
AS26_3N_263_M	5.04				
AS26_3N_265_F	3.92				

Appendix VI. J. QPCR relative quantity (RQ) data for GAPDH2 normalized to PABP1 mRNA expression

Sample name	RQ	Average	SE	Fold change AS11/AS25	Fold change AS26/AS25
AS11_3N_151_F	4.72	11.42	3.29	5.03	3.46
AS11_3N_155_F	25.53				
AS11_3N_156_M	17.53				
AS11_3N_160_F	1.83				
AS11_3N_161_M	16.60				
AS11_3N_162_F	9.48				
AS11_3N_166_M	4.23				
AS25_3N_154_F	2.04	2.27	0.48		
AS25_3N_155_F	4.34				
AS25_3N_156_M	1.64				
AS25_3N_157_M	1.93				
AS25_3N_159_F	1.00				
AS25_3N_160_M	1.40				
AS25_3N_164_F	1.30				
AS25_3N_167_F	4.50				
AS26_3N_253_F	4.98	7.85	1.25		
AS26_3N_254_F	11.06				
AS26_3N_256_M	4.00				
AS26_3N_257_F	12.60				
AS26_3N_260_M	5.80				
AS26_3N_261_F	9.75				
AS26_3N_263_M	10.72				
AS26_3N_265_F	3.84				

Appendix VI. K. QPCR relative quantity (RQ) data for SEPP1 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	1.48	2.93	0.59	1.70	2.83
AS11_3N_155_F	3.90				
AS11_3N_156_M	2.42				
AS11_3N_160_F	1.42				
AS11_3N_161_M	5.74				
AS11_3N_162_F	3.57				
AS11_3N_166_M	1.97				
AS25_3N_154_F	1.58	1.72	0.16		
AS25_3N_155_F	1.83				
AS25_3N_156_M	1.00				
AS25_3N_157_M	1.56				
AS25_3N_159_F	1.48				
AS25_3N_160_M	1.68				
AS25_3N_164_F	2.42				
AS25_3N_167_F	2.24				
AS26_3N_253_F	3.79	4.87	0.96		
AS26_3N_254_F	4.44				
AS26_3N_256_M	4.05				
AS26_3N_257_F	4.92				
AS26_3N_260_M	6.07				
AS26_3N_261_F	10.89				
AS26_3N_263_M	2.15				
AS26_3N_265_F	2.68				

Appendix VI. L. QPCR relative quantity (RQ) data for SEPP2 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	2.15	5.18	1.01	2.92	5.11
AS11_3N_155_F	6.65				
AS11_3N_156_M	6.49				
AS11_3N_160_F	2.44				
AS11_3N_161_M	9.09				
AS11_3N_162_F	6.49				
AS11_3N_166_M	2.94				
AS25_3N_154_F	1.82	1.78	0.31		
AS25_3N_155_F	3.76				
AS25_3N_156_M	1.05				
AS25_3N_157_M	1.78				
AS25_3N_159_F	1.30				
AS25_3N_160_M	1.52				
AS25_3N_164_F	1.00				
AS25_3N_167_F	1.97				
AS26_3N_253_F	11.59	9.06	1.48		
AS26_3N_254_F	9.27				
AS26_3N_256_M	9.09				
AS26_3N_257_F	7.22				
AS26_3N_260_M	13.57				
AS26_3N_261_F	14.68				
AS26_3N_263_M	3.99				
AS26_3N_265_F	3.10				

Appendix VI. M. QPCR relative quantity (RQ) data for NUPR1 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	1.31	1.89	0.25	0.98	2.25
AS11_3N_155_F	1.63				
AS11_3N_156_M	1.83				
AS11_3N_160_F	1.19				
AS11_3N_161_M	3.02				
AS11_3N_162_F	1.72				
AS11_3N_166_M	2.57				
AS25_3N_154_F	2.14	1.94	0.16		
AS25_3N_155_F	2.30				
AS25_3N_156_M	1.29				
AS25_3N_157_M	2.55				
AS25_3N_159_F	1.58				
AS25_3N_160_M	2.33				
AS25_3N_164_F	1.68				
AS25_3N_167_F	1.61				
AS26_3N_253_F	2.46	4.35	1.14		
AS26_3N_254_F	2.54				
AS26_3N_256_M	3.28				
AS26_3N_257_F	4.94				
AS26_3N_260_M	7.88				
AS26_3N_261_F	10.37				
AS26_3N_263_M	1.00				
AS26_3N_265_F	2.33				

Appendix VI. N. QPCR relative quantity (RQ) data for ADAMTS-1 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	11.70	3.33	1.41	1.79	2.37
AS11_3N_155_F	1.55				
AS11_3N_156_M	1.03				
AS11_3N_160_F	2.72				
AS11_3N_161_M	2.45				
AS11_3N_162_F	1.71				
AS11_3N_166_M	2.15				
AS25_3N_154_F	2.29	1.86	0.19		
AS25_3N_155_F	1.17				
AS25_3N_156_M	1.63				
AS25_3N_157_M	1.63				
AS25_3N_159_F	1.49				
AS25_3N_160_M	2.75				
AS25_3N_164_F	2.35				
AS25_3N_167_F	1.56				
AS26_3N_253_F	3.72	4.40	0.64		
AS26_3N_254_F	6.40				
AS26_3N_256_M	5.72				
AS26_3N_257_F	2.71				
AS26_3N_260_M	4.89				
AS26_3N_261_F	4.94				
AS26_3N_263_M	1.00				
AS26_3N_265_F	5.80				

Appendix VI. O. QPCR relative quantity (RQ) data for AA5 normalized to PABP1 mRNA expression					
Sample name	**RQ**	**Average**	**SE**	**Fold change AS11/AS25**	**Fold change AS26/AS25**
AS11_3N_151_F	1.37	1.40	0.19	0.92	1.17
AS11_3N_155_F	1.12				
AS11_3N_156_M	1.10				
AS11_3N_160_F	1.04				
AS11_3N_161_M	2.38				
AS11_3N_162_F	1.79				
AS11_3N_166_M	1.00				
AS25_3N_154_F	1.20	1.53	0.14		
AS25_3N_155_F	2.41				
AS25_3N_156_M	1.28				
AS25_3N_157_M	1.39				
AS25_3N_159_F	1.36				
AS25_3N_160_M	1.68				
AS25_3N_164_F	1.20				
AS25_3N_167_F	1.70				
AS26_3N_253_F	1.86	1.79	0.22		
AS26_3N_254_F	1.55				
AS26_3N_256_M	1.41				
AS26_3N_257_F	2.52				
AS26_3N_260_M	2.08				
AS26_3N_261_F	2.70				
AS26_3N_263_M	1.14				
AS26_3N_265_F	1.03				

APPENDIX VII. Transcripts (46) with greater than 2-fold expression in diploid growth hormone transgenic Atlantic salmon family AS11 in comparison to its triploid counterparts in any 3 out of 4 technical replicated arrays.

EST	Gene Name of Best BLASTX or BLASTN [(N)] Hit	Length (% ID)	E value	Function of Best BLASTX Hit	$\overline{X}$ Fold Change	SE
DW578952	Onmycontig mRNA sequence [EZ775803; *Oncorhynchus mykiss*] [(N)]	491 (89%)	8e-163	Unknown	8.574	6.694
CA053000	Onmycontig mRNA sequence [EZ854926; *Oncorhynchus mykiss*] [(N)]	109 (91%)	1e-31	Unknown	7.391	5.495
EG903061	Unnamed protein product [CAG13897; *Tetraodon nigroviridis*]	237 (53%)	2e-37	Unknown [Q4RCI6]	7.203	5.338
CB516921	Onmycontig mRNA sequence [EZ806257; *Oncorhynchus mykiss*] [(N)]	560 (93%)	0	Unknown	6.948	4.602
EG891229	No significant BLASTX or BLASTN hit	N/A	N/A	Unknown	6.519	2.542
DY712187	Bardet-Biedl syndrome 7 protein [ACN10843; *Salmo salar*]	96 (100%)	3e-47	Unknown [C0H9X4]	6.149	2.321
DY696537	Onmycontig mRNA sequence [EZ825292; *ncorhynchus nerka*] [(N)]	496 (84%)	2e-117	Unknown	6.086	2.238
EG809322	Onmycontig mRNA sequence [EZ853893; *Oncorhynchus mykiss*] [(N)]	503 (90%)	0	Unknown	5.959	3.902
DW572334	Onmycontig mRNA sequence [EZ769629; *Oncorhynchus mykiss*] [(N)]	523 (96%)	0	Unknown	5.002	2.769
EG836006	Onmycontig mRNA sequence [EZ775375; *Oncorhynchus mykiss*] [(N)]	847 (93%)	0	Unknown	4.747	1.630
DW536742	Onmycontig mRNA sequence [EZ781375; *Oncorhynchus mykiss*] [(N)]	516 (97%)	0	Unknown	3.928	1.495
EG928772	Onmycontig mRNA sequence [EZ860178; *Oncorhynchus mykiss*] [(N)]	152 (88%)	1e-40	Unknown	3.441	0.775
FC072752	N-succinyl-L,L-diaminopimelate aminotransferase [CAJ64748; *Frankia alni* ACN14a]	83 (49%)	1e-15	Pyridoxal phosphate binding; Succinyldiaminopimelate transaminase activity (GO:0030170; GO:0009016) [Q0RCS6]	3.231	1.262
DW542830	Unnamed protein product [CAG04255;	149 (81%)	3e-65	ATP binding; DNA photolyase	3.098	0.869

	Tetraodon nigroviridis]			activity; Protein serine/threonine kinase activity (GO:0005524; GO:0003913; GO:0004674) [Q4S527]		
CA051495	Zgc: 65774 [AAH56511; *Danio rerio*]	105 (63%)	1e-19	Unknown [Q6PHL2]	3.032	0.898
DY738897	Genomic sequence [GQ505858; Salmo salar] (N)	387 (87%)	4e-116	RNA binding; Structural constituent of ribosome (GO:0003723; GO:0003735) [A7KIL2]	3.021	0.782
DY695227	Engulfment and cell motility protein 1 putative mRNA [BT045058; *Salmo salar*] (N)	744 (99%)	0	Binding (GO:0005488) [B5X1Y9]	2.944	0.783
CB512354	Mixed_tissue cDNA [*Salmo salar*] (N)	711 (98.5%)	0	Unknown	2.901	0.540
DW545338	Nmycontig mRNA sequence [EZ775280; *Oncorhynchus mykiss*] (N)	725 (91%)	0	Unknown	2.880	0.735
EG880449	Unnamed protein product [CAG01864; *Tetraodon nigroviridis*]	217 (75%)	8e-80	Sequence-specific DNA binding; Transcription factor activity (GO:0043565; GO:0003700) [Q4SBW8]	2.843	0.759
DW546883	No significant BLASTX or BLASTN hit	N/A	N/A	Unknown	2.738	0.621
CB511959	LOC560459 protein [AAI34875; *Danio rerio*]	229 (62%)	6e-83	Transporter activity (GO:0005215) [A4IG10]	2.665	0.594
CA057890	Transmembrane protein 19 [AAH71522; *Danio rerio*]	146 (76%)	1e-50	Cellular component: integral to membrane (GO:0016021) [Q6IQ88]	2.580	0.572
CA052390	Onmycontig mRNA sequence [EZ774413; *Oncorhynchus mykiss*] (N)	702 (85%)	0	Unknown	2.566	0.461
EG886034	Tuberin-like protein 1 splicing variant2 [BAH47606; *Danio rerio*]	50 (80%)	1e-10	GTPase activator activity (GO:0005096) [C0SU62]	2.548	0.605
DW578713	Bcl2 antagonist of cell death putative mRNA [BT060150; *Salmo salar*] (N)	635 (98%)	0	Unknown [B5X1T1]	2.507	0.642
CB510906	MCG53020, isoform CRA_a [EDL18762; *Mus musculus*]	68 (63%)	5e-15	Unknown	2.483	0.387
DY730152	Unnamed protein product [CAG09754;	94 (84%)	1e-41	Unknown [Q4RPC8]	2.415	0.437

	Tetraodon nigroviridis]					
CB515176	MCG56028 [EDL14132; *Mus musculus*]	102 (49%)	7e-12	Unknown	2.365	0.327
CB500771	Onmycontig mRNA sequence [EZ914509; *Oncorhynchus mykiss*] (N)	246 (92%)	2e-89	Unknown	2.343	0.401
CA054654	40 kDa peptidyl-prolyl cis-trans isomerase [ACO07506; *Oncorhynchus mykiss*]	105 (100%)	5e-48	Binding; Peptidyl-prolyl cis-trans isomerase activity (GO:0005488; GO:0003755) [C1BEQ3]	2.293	0.296
DY714544	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor putative mRNA [BT059472; *Salmo salar*] (N)	543 (93%)	0	Isomerase activity (GO:0016853) [C0HAW6]	2.277	0.479
DY739935	Onmycontig mRNA sequence [EZ796884; *Oncorhynchus mykiss*] (N)	461 (91%)	3e-171	Unknown	2.249	0.450
DY701882	Unnamed protein product [CAG00269; *Tetraodon nigroviridis*]	180 (82%)	1e-80	Unknown [Q4SGG3]	2.230	0.206
CA058569	No significant BLASTX or BLASTN hit	N/A	N/A	Unknown	2.229	0.392
CA061505	Onmycontig mRNA sequence [EZ911903; *Oncorhynchus mykiss*] (N)	365 (94%)	3e-156	Unknown	2.217	0.168
CB503293	Vacuolar protein sorting-associated protein 35 putative mRNA [BT059024; *Salmo salar*] (N)	563 (100%)	0	Unknown [C0H9L8]	2.205	0.356
DY695152	Onmycontig mRNA sequence [EZ801276; *Oncorhynchus mykiss*] (N)	224 (92%)	3e-82	Unknown	2.195	0.434
CA058544	Vacuolar proton pump subunit H putative mRNA [BT045050; *Salmo salar*] (N)	640 (98%)	0	Binding; Proton-transporting ATPase activity, rotational mechanism (GO:0005488 GO:0046961) [B5X1Y1]	2.157	0.387
EG802669	Onmycontig mRNA sequence [EZ806707; *Oncorhynchus mykiss*] (N)	311 (88%)	3e-97	Unknown	2.156	0.184
DW557635	Dexamethasone-induced Ras-related protein 1 precursor [ACI66407; *Salmo salar*]	45 (88%)	3e-13	GTP binding; GTPase activity (GO:0005525; GO:0003924) [B5X6D7]	2.152	0.336
DW551849	Phospholipase A-2-activating protein [ACN11010; *Salmo salar*]	41 (100%)	2e-14	Unknown [C0HAE1]	2.151	0.386
DY726321	No significant BLASTX or BLASTN hit	N/A	N/A	Unknown	2.127	0.412

CA041274	Onmycontig mRNA sequence [EZ764537; *Oncorhynchus mykiss*] (N)	570 (91%)	0	Unknown	2.125	0.204
EG871248	Transmembrane protein 185-like putative mRNA [BT046074; *Salmo salar*] (N)	110 (99%)	3e-47	Cellular Component: integral to membrane (GO:0016021) [B5X4V5]	2.082	0.154
CA058955	Onmycontig mRNA sequence [EZ878067; *Oncorhynchus mykiss*] (N)	603 (86%)	4e-170	Unknown	2.076	0.338

See Appendix II for footnotes.

APPENDIX VIII. Transcripts (133) with greater than 2-fold expression in triploid growth hormone transgenic Atlantic salmon family AS11 in comparison to its diploid counterparts in any 3 out of 4 technical replicated arrays.

EST	Gene Name of Best BLASTX or BLASTN (N) Hit	Length (% ID)	E value	Function of best BLASTX Hit	$\bar{X}$ Fold Change	SE
CB485951	HSC71 [AAB21658; *Oncorhynchus mykiss*]	182 (100%)	4e-99	ATP binding (GO:0005524) [P08108]	10.916	4.954
CB511584	Onmycontig mRNA sequence [EZ769635; *Oncorhynchus mykiss*] (N)	196 (92%)	2e-70	Unknown	9.737	7.257
CB493595	Delta5-desaturase-like protein [ABU87822; *Oncorhynchus masou*]	87 (98%)	1e-45	Heme binding; Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [A7XUS7]	8.991	2.478
EG860968	Heat shock 90kDa protein 1 beta isoform b [BAD90024; *Oncorhynchus mykiss*]	204 (98%)	2e-98	ATP binding; Unfolded protein binding (GO:0005524; GO:0051082) [Q5DW65]	7.866	3.410
CA043328	CHK1 checkpoint homolog (S. pombe) [CAJ83813; *Xenopus tropicalis*]	45 (97%)	3e-17	ATP binding; Protein serine/threonine kinase activity (GO:0005524; GO:0004674) [Q28EK6]	7.403	3.313
EG843000	Hypothetical protein [BAF94331; *Fundulus heteroclitus*]	176 (91%)	6e-87	Unknown [A9CQJ8]	7.086	3.811
CB493973	Onmycontig mRNA sequence [EZ905614; *Oncorhynchus mykiss*] (N)	603 (99%)	0	Unknown	7.021	4.303
CA048145	Selenoprotein P, plasma, 1a [AAI59241; *Danio rerio*]	32 (71%)	1e-05	Selenium binding (GO:0008430) [A9JRW5]	6.728	1.982
CA048996	Disulfide-isomerase A4 precursor putative mRNA [BT072419; *Salmo salar*] (N)	245 (97%)	9e-113	Unknown	6.327	4.057
CA051670	Onmycontig mRNA sequence	497 (92%)	0	Unknown	6.292	3.946

	[EZ771031; *Oncorhynchus mykiss*] (N)					
CA055690	Vitellogenin 1 [AAT11177; *Salvelinus alpinus*]	210 (90%)	4e-108	Lipid transporter activity (GO:0005319) [Q6J526]	5.762	1.258
EG780713	Onmycontig mRNA sequence [EZ764240; *Oncorhynchus mykiss*] (N)	604 (85%)	9e-158	Unknown	5.531	1.386
CB494661	Delta5-desaturase-like protein [ABU87822; *Oncorhynchus masou*]	81 (98%)	2e-42	Heme binding; Oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [A7XUS7]	5.427	1.309
EG925336	HCG40021 [EAW75736; *Homo sapiens*]	83 (46%)	2e-16	Unknown	5.419	1.061
CB497762	Onmycontig mRNA sequence [EZ764823; *Oncorhynchus mykiss*] (N)	582 (99%)	0	Unknown	5.406	3.636
CB509791	Zgc: 113828 [AAH96945; *Danio rerio*]	119 (52%)	9e-25	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q4V9D6]	5.373	1.152
CB496584	Alpha actin [AAF75784|AF267496; *Salmo trutta*]	112 (99%)	7e-59	ATP binding; Protein binding (GO:0005524; GO:0005515) [Q9I8K1]	5.132	2.161
EG844708	Calreticulin precursor [ACI33338; *Salmo salar*]	112 (98%)	5e-62	Calcium ion binding; Unfolded protein binding (GO:0005509; GO:0051082) [B5X207]	5.073	1.786
EG872421	CD80-like protein [CAG25516; *Oncorhynchus mykiss*]	106 (69%)	4e-39	Unknown [A1IMH7]	4.611	1.637
DY718129	RNA-binding protein 24-B [ACI33185; *Salmo salar*]	163 (98%)	1e-57	Nucleic acid binding; Nucleotide binding (GO:0003676; GO:0000166) [B5X1K4]	4.609	2.248
CB510761	FBPL4 [ABB29988; *Oncorhynchus mykiss*]	151 (93%)	5e-83	Biological Process: Cell adhesion (GO:0007155) [Q2LK91]	4.548	0.639
EG910790	Tripartite motif-containing protein 25 [ACI68199; *Salmo salar*]	26 (96%)	1e-07	Protein binding; Zinc ion binding (GO:0005515; GO:0008270) [B5XBH9]	4.528	1.306
CA041295	Onmycontig mRNA sequence	395 (91%)	3e-147	Unknown	4.480	1.768

	[EZ854526; *Oncorhynchus mykiss*] (N)					
CA041892	Apolipoprotein A-I precursor [ACI68193; *Salmo salar]*	44 (100%)	7e-16	Lipid binding (GO:0008289) [B5XBH3]	4.161	0.639
CA038381	Onmycontig mRNA sequence [EZ832962; *Oncorhynchus nerka*] (N)	423 (90%)	4e-145	Unknown	3.905	1.563
EG814972	Unknown [ACN31742; *Zea mays*]	79 (70%)	5e-26	Unknown [C0PC47]	3.868	1.314
CB499596	Hydroxysteroid dehydrogenase-like protein 2 [ACN10404|ACN12769; *Salmo salar*]	103 (100%)	7e-40	Oxidoreductase activity; Sterol binding (GO:0016491; GO:0032934) [C0H8N5]	3.781	1.154
DW579486	Profilin-2 [ACI34313|ACM08604; *Salmo salar*]	139 (100%)	9e-77	Actin binding (GO:0003779) [B5X4T2]	3.751	0.976
CB496971	Apolipoprotein A-I-2 [AAB96973; *Oncorhynchus mykiss*]	54 (100%)	5e-14	Lipid binding (GO:0008289) [O57524]	3.739	0.560
CA039027	Glyceraldehyde-3-phosphate dehydrogenase-2 [ACH70939; *Salmo salar*]	64 (100%)	4e-30	NAD or NADH binding; Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5DGR5]	3.698	0.526
CA056648	Nmycontig mRNA sequence [EZ887914; *Oncorhynchus mykiss*] (N)	326 (83%)	1e-75	Unknown	3.619	0.575
CB517225	Vitellogenin 1 [AAT11177; *Salvelinus alpinus*]	211 (90%)	1e-109	Lipid transporter activity (GO:0005319) [Q6J526]	3.610	0.455
CA040124	Selenoprotein Pa precursor putative mRNA [BT072678; *Salmo salar*] (N)	730 (99%)	0	Unknown	3.569	0.345
CB517817	Glutamine synthetase [ACI68482|ACN10326|ACN10517|ACN12686; *Salmo salar*]	99 (100%)	8e-52	Glutamate-ammonia ligase activity (GO:0004356) [B5XCB2]	3.509	0.477
DW584490	Heat shock 70 kDa protein [ACI34374|ACN11053; *Salmo salar*]	126 (99%)	3e-66	ATP binding (GO:0005524) [B5X4Z3]	3.420	0.516
DY699328	Onmycontig mRNA sequence [EZ784933, *Oncorhynchus mykiss*] (N)	573 (91%)	0	Unknown	3.379	0.968
EG803491	Hypothetical protein EHI_101930 [EDS88682; *Entamoeba histolytica* HM-1:IMSS]	41 (85%)	1e-14	Unknown [B1N5S6]	3.369	1.228
CA063745	Onmycontig mRNA sequence	652 (94%)	0	Unknown	3.348	1.129

	[EZ777580; *Oncorhynchus mykiss*] (N)					
CA043170	FBP32 precursor [ABB29989; *Morone saxatilis*]	62 (74%)	1e-20	Biological Process: cell adhesion (GO:0007155) [Q2LK90]	3.335	1.060
CB509933	Complement factor H precursor [CAF25505; *Oncorhynchus mykiss*]	137 (75%)	4e-56	N/A [Q2L4Q6]	3.329	0.114
CA041124	Induced myeloid leukemia cell differentiation protein Mcl-1 homolog putative mRNA [BT072485; *Salmo salar*] (N)	617 (100%)	0	Unknown	3.275	0.899
CA049943	Adenylyl cyclase-associated protein 1 putative mRNA [BT045210; *Salmo salar*] (N)	610 (99%)	0	Actin binding (GO:0003779) [B5X2E1]	3.249	0.826
CB489453	CHK1 checkpoint-like protein [ABK29471; *Helicoverpa armigera*]	47 (91%)	3e-16	Unknown [B6A8G9]	3.242	0.528
CB493972	Sec61 alpha form B [AAK29082|AF346601; *Oncorhynchus mykiss*]	176 (98%)	2e-100	P-P-bond-hydrolysis-driven protein transmembrane transporter activity (GO:0015450) [Q98SN8]	3.242	0.893
EG781579	KIAA1109 [ACN58652; *Salmo salar*]	243 (100%)	5e-128	Unknown [C0PUB8]	3.237	1.104
CB516929	Hypothetical protein BRAFLDRAFT_102843 [EEN53827; *Branchiostoma floridae*]	63 (38%)	2e-10	Unknown [C3Z0S3]	3.171	0.786
CB510516	Onmycontig mRNA sequence [EZ841842; *Oncorhynchus mykiss*] (N)	655 (93%)	0	Unknown	3.141	0.712
CA044192	Sorcin [ACM08665; *Salmo salar*]	97 (100%)	5e-51	Calcium ion binding (GO:0005509) [B9EMB8]	3.107	0.965
CB496430	Onmycontig mRNA sequence [EZ910586; *Oncorhynchus mykiss*] (N)	411 (92%)	2e-158	Unknown	3.081	0.437
CA039874	Plasminogen activator inhibitor 1 RNA-binding protein [ACI33707; *Salmo salar*]	113 (100%)	3e-30	Unknown [B5X326]	3.062	0.972
CA044104	Selenoprotein Pa precursor putative mRNA [BT072678; *Salmo salar*] (N)	684 (99%)	0	Unknown	3.050	0.515
CB494453	Onmycontig mRNA sequence [EZ906468; *Oncorhynchus mykiss*] (N)	411 (90%)	9e-147	Unknown	3.035	0.677
CB510654	Chromosome 20 open reading frame 149	121 (100%)	2e-58	Biological Process:Cell	3.031	0.626

	[ACH70875; *Salmo salar*]			differentiation; Multicellular organismal development (GO:0030154; GO:0007275) [B5DGK1]		
CA055480	No significant BLASTX or BLASTN hit	N/A	N/A	Unknown	3.026	0.884
CB509467	Fumarylacetoacetae [ACO09168; *Osmerus mordax*]	227 (86%)	1e-112	Fumarylacetoacetase activity (GO:0004334) [C1BJG5]	3.000	0.514
CB498890	Tyrosine phosphatase type IVA 2 [ACM08235; *Salmo salar*]	44 (100%)	7e-17	Protein tyrosine/serine/threonine phosphatase activity (GO:0008138) [B9EL38]	2.987	0.706
CA057311	Delta-5 fatty acyl desaturase (D5fad) Gene [GU294485; *Salmo salar*] (N)	606 (100%)	0	Oxidoreductase activity (GO:0016491) [D2Y360]	2.983	0.267
CA041894	Enolase 3-2 [ACH70931; *Salmo salar*]	192 (100%)	4e-98	Magnesium ion binding; Phosphopyruvate hydratase activity (GO:0000287; GO:0004634) [B5DGQ7]	2.953	0.429
CB498021	Heat shock protein hsp90 [AAB49983; *Oncorhynchus tshawytscha*]	138 (89%)	2e-61	ATP binding; Unfolded protein binding (GO:0005524; GO:0051082) [P87397]	2.950	0.681
DY725373	Eggshell protein [CAA04221; *Salmo salar*]	203 (100%)	9e-117	Unknown [O42465]	2.934	0.448
CA060826	Elongation factor 1-alpha 1 [ACN11490; *Salmo salar*]	38 (100%)	2e-11	GTP binding; GTPase activity; Translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	2.903	0.471
CB496785	Carboxylic ester hydrolase [AAA67523; *Salmo salar*]	165 (86%)	2e-84	Carboxylesterase activity (GO:0004091) [Q92149]	2.897	0.756
CA062494	Extracellular matrix protein 1 precursor putative mRNA [BT059193; *Salmo salar*] (N)	569 (94%)	0	Cellular Component: Extracellular space (GO:0005615) [C0HA37]	2.896	0.506
CB494095	Superoxide dismutase putative mRNA [BT073392; *Oncorhynchus mykiss*] (N)	534 (97%)	0	Metal ion binding; Superoxide dismutase activity (GO:0046872; GO:0004784) [C1BFL3]	2.770	0.681
CA041659	Glutamine synthetase [ACI68482;	80 (100%)	5e-40	Glutamate-ammonia ligase	2.763	0.594

	Salmo salar]			activity (GO:0004356) [B5XCB2]		
CB504246	FBP32II precursor [ABB29992; *Morone chrysops*]	153 (67%)	1e-50	Biological Process: cell adhesion (GO:0007155) [Q2LK87]	2.745	0.245
EG910863	Serum albumin 2 [CAA43187; *Salmo salar*]	232 (78%)	9e-97	Lipid binding; Metal ion binding (GO:0008289; GO:0046872) [Q03156]	2.730	0.418
CA045614	Novel protein (im: 7136654) [CAP19604; *Danio rerio*]	71 (92%)	2e-23	Protein binding (GO:0005515) [A8Y5S9]	2.716	0.513
CB492581	Onmycontig mRNA sequence [EZ763734; *Oncorhynchus mykiss*] (N)	634 (99%)	0	Unknown	2.671	0.459
CA040735	PLAC8-like protein 1 putative mRNA [BT072227; *Salmo salar*] (N)	469 (81%)	6e-116	Unknown	2.666	0.252
CB490586	Nuclear protein 1 [ACI68567; *Salmo salar*]	74 (90%)	3e-36	Unknown [B5XCJ7]	2.664	0.197
CB501971	Onmycontig mRNA sequence [EZ776115; *Oncorhynchus mykiss*] (N)	362 (93%)	6e-153	Unknown	2.661	0.648
CB518086	Transposase [AAP49009; *Rana pipiens*]	78 (50%)	6e-17	DNA binding; Transposase activity (GO:0003677; GO:0004803) [Q6X1Z4]	2.660	0.554
CB494413	Onmycontig mRNA sequence [EZ768185; *Oncorhynchus mykiss*] (N)	706 (98%)	0	Unknown	2.658	0.574
CA044731	Stress-associated endoplasmic reticulum protein 1 [ACI68699; *Salmo salar*]	66 (100%)	2e-29	Unknown [B5XCX9]	2.657	0.561
CB514703	DnaJ homolog subfamily C member 3 precursor [ACI34340; *Salmo salar*]	243 (100%)	1e-139	Heat shock protein binding (GO:0031072) [B5X4V9]	2.648	0.668
CX029886	Unnamed protein product [CAF98889; *Tetraodon nigroviridis*]	176 (40%)	4e-23	Growth factor activity (GO:0008083) [Q4SKE3]	2.647	0.626
EG853635	Glycine cleavage system H protein, mitochondrial precursor [ACN10330; *Salmo salar*]	172 (93%)	3e-86	Lipoic acid binding (GO:0031405) [C0H8G1]	2.644	0.231
EG861018	Glucose-6-phosphate-1-dehydrogenase [ABQ42203; *Oncorhynchus mykiss*]	107 (99%)	3e-58	Binding; Glucose-6-phosphate dehydrogenase activity (GO:0005488; GO:0004345) [A5JNM0]	2.625	0.582
CA055102	Transmembrane protein 106B	190 (100%)	3e-81	Integral to membrane	2.611	0.362

	[ACI69652; *Salmo salar*]			(GO:0016021) [B5XFN2]		
CB511111	Novel protein similar to human and mouse ADP-ribosylation factor-like 14 (ARL14) [CAX13605; *Danio rerio*]	112 (54%)	1e-24	GTP binding (GO:0005525) [B8JLB2]	2.605	0.400
CA041067	5-aminolevulinate synthase, erythroid-specific, mitochondrial precursor [ACN10630; *Salmo salar*]	30 (100%)	3e-10	5-aminolevulinate synthase activity; Pyridoxal phosphate binding; Transferase activity, transferring nitrogenous groups (GO:0003870; GO:0030170; GO:0016769) [C0H9B1]	2.603	0.228
CA038129	Onmycontig mRNA sequence [EZ847363; *Oncorhynchus mykiss*] (N)	285 (88%)	3e-93	Unknown	2.595	0.478
CB506406	Onmycontig mRNA sequence [EZ817404; *Oncorhynchus nerka*] (N)	668 (83%)	0	Unknown	2.593	0.549
CB498760	Zinc finger protein 180, isoform CRA_a [EDM08120; *Rattus norvegicus*]	88 (70%)	2e-36	Unknown	2.585	0.606
CA058605	Onmycontig mRNA sequence [EZ766617; *Oncorhynchus mykiss*] (N)	702 (92%)	0	Unknown	2.572	0.415
CA053571	Flavin reductase [ACI67715; *Salmo salar*]	82 (100%)	1e-41	Unknown [B5XA45]	2.565	0.324
CK990607	Complement C1q-like protein 4 precursor [ACM09542; *Salmo salar*]	101 (45%)	2e-18	Unknown [B9EPU5]	2.553	0.510
CB497380	Onmycontig mRNA sequence [EZ905653; *Oncorhynchus mykiss*] (N)	620 (99%)	0	Unknown	2.508	0.522
EG892265	IgH locus B genomic sequence [GU129140; *Salmo salar*] (N)	701 (98%)	0	Unknown	2.501	0.492
CB494587	Glutathione peroxidase type 2 [AAV32968; *Oncorhynchus mykiss*]	71 (84%)	3e-28	Glutathione peroxidase activity (GO:0004602) [Q5UTE7]	2.497	0.563
CB490824	Notchless protein homolog 1 [ACN58698; *Salmo salar*]	67 (100%)	1e-32	Unknown [C0PUL3]	2.487	0.130
CA039685	Catechol-O-methyltransferase domain-containing protein 1 [ACI69067; *Salmo salar*]	85 (92%)	2e-60	O-methyltransferase activity (GO:0008171) [B5XDZ7]	2.454	0.090
CA060261	Onmycontig mRNA sequence [EZ852424; *Oncorhynchus mykiss*] (N)	534 (92%)	0	Unknown	2.437	0.580
CA051860	Sodium/potassium-transporting ATPase	647 (100%)	0	Sodium:potassium-exchanging	2.433	0.198

	subunit beta-233 putative mRNA [BT059333; *Salmo salar*] (N)			ATPase activity (GO:0005391) [C0HAH7]		
CB510372	Spartin [ACN10853; *Salmo salar*]	217 (94%)	8e-107	Unknown [C0H9Y4]	2.410	0.059
CA043764	Glycine cleavage system H protein, mitochondrial precursor [ACN10330; *Salmo salar*]	79 (100%)	6e-38	Lipoic acid binding (GO:0031405) [C0H8G1]	2.407	0.385
CB492498	Crystallin gamma M2b [ACL98110; *Epinephelus coioides*]	70 (80%)	1e-26	Unknown [B9V3T5]	2.400	0.245
CA063864	Onmycontig mRNA sequence [EZ811233; *Oncorhynchus mykiss*] (N)	513 (93%)	0	Unknown	2.398	0.329
CX282250	Unnamed protein product [CAG08548; *Tetraodon nigroviridis*]	188 (85%)	1e-92	ATP binding; Zinc ion binding (GO:0005524 GO:0008270) [Q4RST4]	2.383	0.121
CA061418	Onmycontig mRNA sequence [EZ829065; *Oncorhynchus nerka*] (N)	674 (74%)	2e-128	Unknown	2.371	0.282
CA040315	Onmycontig mRNA sequence [EZ764761; *Oncorhynchus mykiss*] (N)	529 (95%)	0	Unknown	2.350	0.257
CA058336	Transforming growth factor-beta-induced protein ig-h3 precursor [ACI34040; *Salmo salar*]	46 (84%)	7e-12	Unknown	2.334	0.245
CB490371	Putative H3 histone family 3B variant 1 [ACH46259; *Taeniopygia guttata*]	79 (89%)	1e-33	DNA binding (GO:0003677) [B5G4P8]	2.332	0.451
CA041476	Hypothetical protein CHGG_10452 [EAQ84048; *Chaetomium globosum* CBS 148.51]	112 (34%)	5e-08	Transcription factor activity; Zinc ion binding (GO:0003700; GO:0008270) [Q2GNK2]	2.327	0.081
CA770640	Onmycontig mRNA sequence [EZ914073; *Oncorhynchus mykiss*] (N)	569 (93%)	0	Unknown	2.324	0.326
CB496558	Proteasome maturation protein [ACO08214; *Oncorhynchus mykiss*]	142 (99%)	2e-73	Cellular Component: Proteasome complex (GO:0000502) [C1BGR1]	2.312	0.402
EG936318	No significant BLASTX or BLASTN hit	N/A	N/A	Unknown	2.301	0.255
CK991349	Onmycontig mRNA sequence [EZ782390; *Oncorhynchus mykiss*] (N)	465 (98%)	0	Unknown	2.245	0.340
CB514053	Programmed cell death protein 10 [ACM08980; *Salmo salar*]	52 (100%)	3e-21	Unknown [B9EN83]	2.238	0.328

CK990267	Onmycontig mRNA sequence [EZ796597; *Oncorhynchus mykiss*] (N)	351 (82%)	1e-98	Unknown	2.231	0.226
CA049880	Receptor expression-enhancing protein 5 [ACM09747; *Salmo salar*]	189 (98%)	3e-82	Receptor activity (GO:0004872) [B9EQF0]	2.225	0.166
DY727935	Novel protein similar to vertebrate leucine-rich repeats and calponin homology (CH) domain containing family [CAM56750; *Danio rerio*]	114 (77%)	3e-39	Protein binding (GO:0005515) [A3QJZ8]	2.216	0.275
CB496576	Beta-2-microglobulin precursor [ACO15545; *Caligus clemensi*]	93 (100%)	6e-50	Cellular Component: MHC class I protein complex (GO:0042612) [C1C2P2]	2.209	0.250
CB497579	Glutathione S-transferase [BAA76974; *Oncorhynchus nerka*]	159 (96%)	4e-84	Glutathione transferase activity (GO:0004364) [Q9W647]	2.182	0.197
CA050836	Onmycontig mRNA sequence [EZ791609; *Oncorhynchus mykiss*] (N)	703 (94%)	0	Unknown	2.178	0.225
EG910206	Depdc6-003 [ACD12872; *Mus musculus*]	147 (70%)	9e-41	Protein binding (GO:0005515) [B2ZRS8]	2.144	0.157
EG793488	Membrane-spanning 4-domains subfamily A member 4A [ACI69003; *Salmo salar*]	200 (78%)	2e-70	Cellular Component: Integral to membrane (GO:0016021) [B5XDT3]	2.135	0.227
DW537030	Thioredoxin domain-containing protein 5 precursor putative mRNA [BT072052; *Salmo salar*] (N)	658 (98%)	0	Unknown	2.134	0.417
CB498020	Onmycontig mRNA sequence [EZ763824; *Oncorhynchus mykiss*] (N)	578 (97%)	0	Unknown	2.131	0.359
CA058002	Polypeptide N-acetylgalactosaminyltransferase 6 putative mRNA [BT072542; *Salmo salar*] (N)	739 (99%)	0	Unknown	2.125	0.319
CA060485	Transcription factor PU.1 [ACI67276; *Salmo salar*]	129 (100%)	1e-70	Sequence-specific DNA binding; Transcription factor activity (GO:0043565; GO:0003700) [B5X8V6]	2.096	0.159
CB497206	Onmycontig mRNA sequence [EZ763908; *Oncorhynchus mykiss*] (N)	660 (99%)	0	Unknown	2.095	0.203
CA045270	U3 small nucleolar ribonucleoprotein protein IMP4 [ACI66547; *Salmo*	205 (99%)	6e-113	Nucleic acid binding (GO:0003676) [B5X6S7]	2.087	0.302

	salar]					
CB507829	Onmycontig mRNA sequence [EZ824458; *Oncorhynchus mykiss*] (N)	534 (92%)	0	Unknown	2.062	0.129
CA039910	mRNA for simple type II keratin K8a [AJ272373; *Oncorhynchus mykiss*] (N)	665 (97%)	0	Structural molecule activity (GO:0005198) [Q90YH3]	2.046	0.308
CB515951	Onmycontig mRNA sequence [EZ825789; *Oncorhynchus nerka*] (N)	718 (87%)	0	Unknown	2.039	0.368
EG851555	Novel cds [BT072567; *Salmo salar*] (N)	846 (100%)	0	Unknown	2.034	0.296
CB511208	Fast myotomal muscle actin [AAG25672|AF304406; *Salmo salar*]	138 (100%)	8e-75	ATP binding; protein binding (GO:0005524; GO:0005515) [Q78BU2]	2.004	0.247
CA063008	High affinity copper uptake protein 1 putative mRNA [BT059358; *Salmo salar*] (N)	714 (99%)	0	Copper ion transmembrane transporter activity (GO:0005375) [C0HAK2]	1.972	0.320
DY721630	Onmycontig mRNA sequence [EZ888359; *Oncorhynchus mykiss*] (N)	318 (77%)	2e-65	Unknown	1.968	0.291
EG880619	TSC22 domain family protein 3 [ACI34064; *Salmo salar*]	40 (95%)	4e-13	Transcription factor activity (GO:0003700) [B5X433]	1.950	0.296
CB501928	Carbonic anhydrase putative mRNA [BT058764; *Salmo salar*] (N)	600 (99%)	0	Carbonate dehydratase activity; zinc ion binding (GO:0004089; GO:0008270) [B5X3I8]	1.912	0.123

See Appendix II for footnotes.

APPENDIX IX. Transcripts (17) with greater than 2-fold expression in diploid growth hormone transgenic Atlantic salmon family AS25 in comparison to its triploid counterparts in any 3 out of 4 technical replicated arrays.

EST	Gene Name of Best BLASTX or BLASTN (N) Hit	Length (% ID)	E value	Function of Best BLASTX Hit	$\bar{X}$ Fold Change	SE
CB496919	Glycerol-3-phosphate dehydrogenase [AAK07737; *Salmo salar*]	36 (97%)	8e-14	NAD or NADH binding (GO:0051287) [Q98SJ9]	4.595	2.216
CA053890	Hypothetical protein MGC146992 [AAI21550; *Xenopus (Silurana) tropicalis*]	155 (41%)	4e-26	Nucleic acid binding (GO:0003676) [Q0V9I0]	4.590	2.420
CA051169	Onmycontig mRNA sequence [EZ763914; *Oncorhynchus nerka*] (N)	485 (91%)	0	Unknown	4.367	1.320
CB500430	Hepcidin-1 precursor [ACI67048; *Salmo salar*]	34 (94%)	1e-15	Cellular Component: Extracellular region (GO:0005576) [B5X878]	4.340	2.298
CB503834	Unknown large open reading frame mRNA [BT072179; *Salmo salar*] (N)	99 (100%)	1e-43	Unknown	3.919	1.140
CA037891	Leukocyte cell-derived chemotaxin 2 precursor [ACI68507; *Salmo salar*]	55 (100%)	2e-25	Unknown [B5XCD7]	3.729	0.597
EG928348	Unnamed protein product [CAF98477; *Tetraodon nigroviridis*]	246 (29%)	1e-26	Unknown [Q4SLK5]	3.591	0.369
EG929236	Stannin [ACN10806; *Salmo salar*]	87 (100%)	1e-31	Unknown [C0H9T7]	3.330	0.204
CB486904	40S ribosomal protein S3 [ACI67079; *Salmo salar*]	137 (100%)	3e-70	RNA binding (GO:0003723) [B5X8A9]	3.104	0.877
CK991068	Hepcidin-1 precursor [ACI67048; *Salmo salar*]	31 (93%)	2e-13	Cellular Component: Extracellular region (GO:0005576) [B5X878]	3.045	0.527
DW569180	Onmycontig mRNA sequence [EZ764712; *Oncorhynchus mykiss*]	587 (91%)	0	Unknown	2.799	0.165
CB499145	B-cell receptor-associated protein 31 putative mRNA [BT045436; *Salmo salar*]	203 (100%)	2e-101	Receptor activity (GO:0004872) [B5X317]	2.750	0.469

CA050886	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*]	157 (100%)	8e-85	NAD or NADH binding (GO:0051287) [B5XG76]	2.428	0.413
DY731837	Onmycontig mRNA sequence [EZ769153; *Oncorhynchus mykiss*] (N)	464 (85%)	1e-127	Unknown	2.287	0.257
DW567850	Acyl-CoA-binding protein putative mRNA [BT049229; *Salmo salar*] (N)	405 (90%)	1e-146	Acyl-CoA binding (GO:0000062) [B5XDW0]	2.245	0.143
CB510338	Histone H2A.x [ACN09953; *Salmo salar*]	121 (100%)	1e-47	DNA binding (GO:0003677) [B5X5B2]	2.226	0.195
CB510992	Apolipoprotein A-IV precursor [ACI67068; *Salmo salar*]	97 (96%)	2e-44	Lipid binding (GO:0008289) [B5X898]	2.119	0.163

See Appendix II for footnotes.

APPENDIX X. Transcripts (18) with greater than 2-fold expression in triploid growth hormone transgenic Atlantic salmon family AS25 in comparison to its diploid counterparts in any 3 out of 4 technical replicated arrays.

EST	Gene Name of Best BLASTX or BLASTN (N) Hit	Length (% ID)	E value	Function of Best BLASTX Hit	$\bar{X}$ Fold Change	SE
CB496629	Thioredoxin-dependent peroxide reductase, mitochondrial precursor [ACI69558; *Salmo salar*]	108 (99%)	8e-77	Antioxidant activity; Oxidoreductase activity (GO:0016209; GO:0016491) [B5XFD8]	5.380	2.771
CA041811	Transducin (beta)-like 2 [AAH65682; *Danio rerio*]	147 (71%)	3e-58	Unknown [Q6P0B5]	4.691	2.589
CB494491	Onmycontig mRNA sequence [EZ786281; *Oncorhynchus mykiss*]	700 (97%)	0	Unknown	3.532	1.103
CB517225	Vitellogenin 1 [AAT11177; *Salvelinus alpinus*]	211 (90%)	1e-109	Lipid transporter activity (GO:0005319) [Q6J526]	3.484	0.320
CB515390	Vitellogenin 1 [AAT11177; *Salvelinus alpinus*]	46 (73%)	3e-07	Lipid transporter activity (GO:0005319) [Q6J526]	2.929	0.684
CA061076	Onmycontig mRNA sequence [EZ767413; *Oncorhynchus mykiss*] (N)	556 (91%)	0	Unknown	2.718	0.707
DY721363	SRC-like-adapter putative mRNA [BT044892; *Salmo salar*] (N)	578 (97%)	0	Protein binding (GO:0005515) [B5X1H3]	2.683	0.778
EG937869	Unnamed protein product [CAG03989; *Tetraodon nigroviridis*]	107 (59%)	2e-23	Unknown [Q4S5U3]	2.474	0.518
CB515643	Ig kappa chain V-IV region JI precursor [ACI70072; *Salmo salar*]	153 (96%)	6e-83	Unknown	2.470	0.572
CA064135	Vigilin [ACN10888; *Salmo salar*]	90 (98%)	4e-42	RNA binding (GO:0003723) [C0HA19]	2.419	0.468
DY708641	FKIAA0680 [AAC60292; *Takifugu rubripes*]	50 (46%)	3e-07	Protein binding; ubiquitin-protein ligase activity; zinc ion binding (GO:0005515; GO:0004842; GO:0008270) [O42498]	2.369	0.401
CB510998	Novel protein [CAX14664; *Danio rerio*]	85 (49%)	3e-09	Unknown [B8JHY9]	2.334	0.428
EG787440	Alpha-actinin [AAN77132; *Danio rerio*]	139 (82%)	2e-59	Actin binding; calcium ion binding (GO:0003779;	2.184	0.467

				GO:0005509) [Q8AX99]		
DW548924	Onmycontig mRNA sequence [EZ799290; *Oncorhynchus mykiss*] (N)	507 (89%)	7e-173	Unknown	2.170	0.363
CB509433	Protein gamma-1 putative mRNA [BT059187; *Salmo salar*] (N)	351 (89%)	2e-119	Protein domain specific binding (GO:0019904) [C0HA31]	2.122	0.203
CA055196	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial precursor putative mRNA [BT049908; *Salmo salar*] (N)	601 (99%)	0	Iron ion binding; iron-sulfur cluster binding; protein binding (GO:0005506; GO:0051536; GO:0005515) [B5XFT9]	2.022	0.232
CB517029	ATP-citrate synthase putative mRNA [BT072721; *Salmo salar*] (N)	722 (99%)	0	Unknown	1.980	0.169
EG819175	Glutathione S-transferase alpha 3 [ACI66699; *Salmo salar*]	161 (97%)	8e-84	Glutathione transferase activity (GO:0004364) [B5X779]	1.970	0.318

See Appendix II for footnotes.

APPENDIX XI. Transcripts (124) with greater than 2-fold expression in diploid growth hormone transgenic Atlantic salmon family AS29 in comparison to its triploid counterparts in any 3 out of 4 technical replicated arrays.

EST	Gene Name of Best BLASTX or BLASTN (N) Hit	Length (% ID)	E value	Function of Best BLASTX Hit	$\bar{X}$ Fold Change	SE
EG913435	Onmycontig mRNA sequence [EZ807050; *Oncorhynchus mykiss*] (N)	305 (93%)	8e-119	Unknown	5.545	2.913
CA054194	Unknown			Unknown	4.900	2.842
EG941860	Onmycontig mRNA sequence [EZ834937; *Oncorhynchus nerka*] (N)	569 (92%)	0	Unknown	4.335	1.554
CX257515	BCL-WAV [ADB55705; *Danio rerio*]	136 (68%)	6e-44	Biological Process: regulation of apoptosis (GO:0042981) [D2Y5Q2]	4.149	0.725
CA055066	Unnamed protein product [CAF90322; *Tetraodon nigroviridis*]	93 (90%)	9e-37	Sequence-specific DNA binding transcription factor activity; zinc ion binding (GO:0003700; GO:0008270) [Q4T9W0]	4.115	0.819
EG913553	Tripartite motif-containing protein 16 [ACI34059; *Salmo salar*]	152 (77%)	3e-62	Protein binding; zinc ion binding (GO:0005515; GO:0008270) [B5X428]	4.101	0.758
DY739903	Unknown			Unknown	3.789	1.228
DW557166	Onmycontig mRNA sequence [EZ902546; *Oncorhynchus mykiss*] (N)	80 (94%)	1e-22	Unknown	3.653	1.289
EG911879	Predicted protein [EDO45690; *Nematostella vectensis*]	159 (34%)	9e-17	Unknown [A7RS65]	3.629	0.389
CA043380	LAG1 longevity assurance homolog 2 [ACO09885; *Osmerus mordax*]	112 (59%)	7e-24	Sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity (GO:0043565; GO:0003700) [C1BLI2]	3.480	0.248
EG888926	Structural maintenance of chromosomes 1B [CAQ08672; *Homo sapiens*]	40 (75%)	2e-10	ATP binding; protein binding (GO:0005524; GO:0005515)	3.455	0.106

				[Q8NDV3]		
DY734333	Tripartite motif-containing protein 16 [ACI34059; *Salmo salar*]	74 (76%)	1e-26	Protein binding; zinc ion binding (GO:0005515; GO:0008270) [B5X428]	3.446	0.498
DY734211	Unnamed protein product [CAG06263; *Tetraodon nigroviridis*]	89 (79%)	6e-23	Protein binding (GO:0005515) [Q4RZB9]	3.441	0.242
CA364373	Onmycontig mRNA sequence [EZ831450; *Oncorhynchus nerka*] (N)	476 (98%)	0	Unknown	3.326	0.555
CN442531	Cytochrome c oxidase subunit III [BAG69265; *Iso hawaiiensis*]	133 (91%)	2e-55	Cytochrome-c oxidase activity (GO:0004129) [B5BQ78]	3.294	0.983
CK990279	ADAMTS-1 protein [BAE16358; *Oryzias latipes*]	148 (72%)	4e-59	Metalloendopeptidase activity; zinc ion binding (GO:0004222; GO:0008270) [Q4AED3]	3.218	0.709
CA061444	Onmycontig mRNA sequence [EZ792797; *Oncorhynchus mykiss*] (N)	747 (85%)	0	Unknown	3.138	1.045
DY733125	Novel protein similar to vertebrate LIM homeobox 9 [CAK04966; *Danio rerio*]	229 (93%)	1e-113	Sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity; zinc ion binding (GO:0043565; GO:0003700; GO:0008270) [Q1LWV4]	3.130	1.118
DY739738	LOC560459 protein [AAI34875; *Danio rerio*]	162 (67%)	3e-60	Transporter activity (GO:0005215) [A4IG10]	3.084	1.140
EG916263	Unnamed protein product [CAG05465; *Tetraodon nigroviridis*]	230 (61%)	8e-76	Biological Process: signal transduction (GO:0007165) [Q4S1L7]	3.081	0.455
CA056824	Onmycontig mRNA sequence [EZ777208; *Oncorhynchus mykiss*] (N)	540 (86%)	2e-135	Unknown	3.038	0.604
CA039985	Musculoaponeurotic fibrosarcoma oncogene-like mRNA [BT043547; *Salmo salar*] (N)	615 (100%)	0	Sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity (GO:0043565; GO:0003700) [B5DFY8]	3.002	0.565
DW539453	Unknown			Unknown	2.997	0.500
EG765364	Onmycontig mRNA sequence [EZ851328; *Oncorhynchus mykiss*] (N)	167 (92%)	6e-55	Unknown	2.956	0.335

EG898719	Novel protein similar to H.sapiens LYST, lysosomal trafficking regulator [CAX13573; *Danio rerio*]	200 (93%)	6e-107	Unknown [B7ZCY9]	2.919	0.707
DY733596	Onmycontig mRNA sequence [EZ806691; *Oncorhynchus mykiss*] (N)	687 (91%)	0	Unknown	2.876	0.386
CA037891	Leukocyte cell-derived chemotaxin 2 precursor [ACI68507; *Salmo salar*]	55 (100%)	2e-25	Unknown [B5XCD7]	2.868	0.319
CA369300	Onmycontig mRNA sequence [EZ774517; *Oncorhynchus mykiss*] (N)	701 (99%)	0	Unknown	2.862	0.616
CK990943	Unknown			Unknown	2.820	0.084
CX034900	Onmycontig mRNA sequence [EZ901676; *Oncorhynchus mykiss*] (N)	348 (99%)	5e-170	Unknown	2.791	0.478
CB518113	Onmycontig mRNA sequence [EZ909514; *Oncorhynchus mykiss*] (N)	162 (88%)	2e-44	Unknown	2.782	0.886
CB506531	BAC clone RP23-27C10 from chromosome 1 [AC125377; *Mus musculus*] (N)	403 (97%)	0	Unknown	2.774	0.544
EG819717	Onmycontig mRNA sequence [EZ865755; *Oncorhynchus mykiss*] (N)	407 (81%)	9e-68	Unknown	2.757	0.190
CB505381	BAC S0188I22 [DQ156150; *Salmo salar*] (N)	513 (90%)	1e-176	Metal ion binding (GO:0046872) [Q0H917]	2.705	0.521
CB515741	Tetraspanin-8 [ACI68451; *Salmo salar*]	94 (96%)	1e-51	Cellular Component: integral to membrane (GO:0016021) [B5XC81]	2.690	0.267
DW562703	KIAA0415 [ACN11261; *Salmo salar*]	178 (100%)	5e-88	Unknown [C0HB42]	2.688	0.262
DY703407	Zgc: 136564 protein [AAI15181; *Danio rerio*]	77 (67%)	5e-23	Unknown [A4FUL9]	2.680	0.276
DY720073	Unknown			Unknown	2.658	0.216
CX244681	Onmycontig mRNA sequence [EZ805068; *Oncorhynchus mykiss*] (N)	469 (98%)	0	Unknown	2.653	0.379
EG901947	Fermitin family homolog 3 [ACI33779; *Salmo salar*]	89 (98%)	5e-45	Unknown [B5X398]	2.612	0.269
CB501435	Unknown			Unknown	2.598	0.176

CB500771	Onmycontig mRNA sequence [EZ914509; *Oncorhynchus mykiss*] (N)	246 (93%)	2e-89	Unknown	2.595	0.090
DW554007	Unknown			Unknown	2.591	0.471
EG849106	Claudin 28b [ACK86563; *Oncorhynchus mykiss*]	175 (99%)	4e-68	Structural molecule activity (GO:0005198) [C7S8F2]	2.569	0.300
DW581114	Onmycontig mRNA sequence [EZ786153; *Oncorhynchus mykiss*] (N)	301 (93%)	1e-115	Unknown	2.563	0.588
CB498277	Onmycontig mRNA sequence [EZ795018; *Oncorhynchus mykiss*] (N)	423 (99%)	0	Unknown	2.555	0.265
EG924696	Unnamed protein product [CAF97655; *Tetraodon nigroviridis*]	60 (65%)	1e-15	Protein binding (GO:0005515) [Q4SNX7]	2.553	0.547
CK990330	Onmycontig mRNA sequence [EZ833691; *Oncorhynchus nerka*] (N)	383 (92%)	2e-147	Unknown	2.528	0.101
CB508625	Serine/threonine-protein phosphatase 4 regulatory subunit 1-like putative mRNA [BT072802; *Salmo salar*] (N)	244 (90%)	2e-78	Unknown	2.524	0.312
CA064115	Glomulin, like [CAQ13681; *Danio rerio*]	117 (74%)	9e-39	Unknown [B0UYH7]	2.522	0.445
CA062415	Onmycontig mRNA sequence [EZ823781; *Oncorhynchus nerka*] (N)	312 (92%)	9e-116	Unknown	2.521	0.424
CA055113	Onmycontig mRNA sequence [EZ770909; *Oncorhynchus mykiss*] (N)	480 (93%)	0	Unknown	2.503	0.523
CA053623	Cathepsin S precursor [ACN12762; *Salmo salar*]	128 (100%)	5e-73	Cysteine-type endopeptidase activity (GO:0004197) [C0HDJ6]	2.493	0.344
DW541438	Gamma-aminobutyric-acid receptor rho-1A subunit precursor [AAD17894; *Morone americana*]	30 (90%)	9e-09	Extracellular ligand-gated ion channel activity; receptor activity (GO:0005230; GO:0004872) [Q9YGQ4]	2.483	0.386
CA044652	Onmycontig mRNA sequence [EZ906396; *Oncorhynchus mykiss*] (N)	269 (92%)	1e-95	Unknown	2.476	0.298
DW539321	Onmycontig mRNA sequence [EZ768373; *Oncorhynchus mykiss*] (N)	500 (84%)	3e-121	Unknown	2.466	0.192
CA769180	Unknown			Unknown	2.459	0.186
CA041294	Onmycontig mRNA sequence	73 (94%)	4e-20	Unknown	2.446	0.286

	[EZ896737; *Oncorhynchus mykiss*] (N)					
DW535706	Onmycontig mRNA sequence [EZ836478; *Oncorhynchus nerka*] (N)	482 (89%)	2e-158	Unknown	2.428	0.215
DY726715	Creatine kinase, mitochondrial 1 [AAH48050; *Danio rerio*]	86 (76%)	2e-50	ATP binding; kinase activity (GO:0005524; GO:0016301) [Q7ZUN7]	2.427	0.443
DY696138	Onmycontig mRNA sequence [EZ820222; *Oncorhynchus nerka*] (N)	616 (96%)	0	Unknown	2.426	0.196
CA050387	Xaa-Pro aminopeptidase 3 [ACI33098; *Salmo salar*]	86 (100%)	8e-43	Aminopeptidase activity; manganese ion binding (GO:0004177; GO:0030145) [B5X1B7]	2.424	0.295
DW568996	Unknown large open reading frame mRNA [BT072506; *Salmo salar*] (N)	269 (99%)	1e-135	Unknown	2.417	0.231
CB506393	Cytosolic sulfotransferase 2 [ACI66365; *Salmo salar*]	184 (100%)	2e-107	Sulfotransferase activity (GO:0008146) [B5X695]	2.409	0.213
CA057765	Glutamate-rich WD repeat containing 1 [AAH78350; *Danio rerio*]	170 (89%)	2e-86	Unknown [Q6DBV2]	2.396	0.374
CA046002	Interferon-inducible GTPase_b and interferon-inducible GTPase_a genes [EU221179; *Salmo salar*] (N)	225 (99%)	1e-106	GTP binding; hydrolase activity, acting on acid anhydrides (GO:0005525; GO:0016817) [A8WCJ8]	2.377	0.287
CA061939	Onmycontig mRNA sequence [EZ829890; *Oncorhynchus nerka*] (N)	459 (95%)	0	Unknown	2.377	0.224
CX246608	Phosphatidylinositol glycan, class K [AAH71379; *Danio rerio*]	114 (97%)	8e-60	Cysteine-type endopeptidase activity (GO:0004197) [Q6IQM5]	2.376	0.235
CB500533	Onmycontig mRNA sequence [EZ906741; *Oncorhynchus mykiss*] (N)	375 (91%)	4e-126	Unknown	2.375	0.144
CA062412	HtrA serine peptidase 1 [AAH74069; *Danio rerio*]	52 (81%)	2e-16	Insulin-like growth factor binding; serine-type endopeptidase activity (GO:0005520; GO:0004252) [Q6GMI0]	2.367	0.468
DY724226	Onmycontig mRNA sequence [EZ907053; *Oncorhynchus mykiss*] (N)	651 (94%)	0	Unknown	2.364	0.102
DW546771	Ubiquitin-like protein FUBI putative	109 (98%)	3e-43	Structural constituent of ribosome	2.364	0.487

	mRNA [BT057566; *Salmo salar*] (N)			(GO:0003735) [B5DGJ7]		
CB512155	Unnamed protein product [CAF88944; *Tetraodon nigroviridis*]	34 (80%)	5e-08	Unknown [Q4TDT8]	2.363	0.270
EG889014	MHC Class I gene, Sasa-UBA*0601 allele; and proteasome subunit beta type 8, proteasome subunit beta type 10, PSMB9a-like, proteosome subunit beta type 9, transporter 2 ATP binding cassette, bromodomain containing 2, collagen Type XI Alpha2, retinoid X receptor beta, solute carrier 39 (zinc transporter) member 7, and reverse transcriptase-like protein genes [EF210363; *Salmo salar*] (N)	311 (85%)	3e-73	Threonine-type endopeptidase activity (GO:0004298) [A7KE01]	2.363	0.291
EG802849	Sorting nexin-18 [ACN11167; *Salmo salar*]	150 (99%)	8e-60	Phosphoinositide binding; protein binding (GO:0035091; GO:0005515) [C0HAU8]	2.357	0.496
DY733987	Onmycontig mRNA sequence [EZ802768; *Oncorhynchus mykiss*] (N)	492 (89%)	8e-168	Unknown	2.355	0.302
EG904577	BAC CH214-397C7 [AC203456; *Salmo salar*] (N)	401 (89%)	2e-128	Unknown	2.347	0.183
DY713963	Beta-ureidopropionase putative mRNA [BT056453; *Salmo salar*] (N)	257 (99%)	3e-127	Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds (GO:0016810) [B9ELC8]	2.342	0.077
CK990405	Creatine kinase, mitochondrial 2 (ckmt2) mRNA [BT043498; *Salmo salar*] (N)	372 (99%)	0	ATP binding; kinase activity (GO:0005524; GO:0016301) [B5DFT9]	2.338	0.485
DW547292	Retrotransposable element Tf2 155 kDa protein type 3 putative mRNA [BT071928; *Salmo salar*] (N)	724 (100%)	0	DNA binding (GO:0003677) [C0PU14]	2.335	0.328
CA040690	Onmycontig mRNA sequence [EZ906305; *Oncorhynchus mykiss*] (N)	224 (92%)	2e-74	Unknown	2.305	0.233
DW546395	Novel protein similar to vertebrate structural maintenance of chromosomes 6 [CAN88051; *Danio rerio*]	43 (80%)	1e-12	ATP binding (GO:0005524) [A5PN27]	2.302	0.101

CA063338	Onmycontig mRNA sequence [EZ835434; *Oncorhynchus nerka*] (N)	543 (85%)	1e-131	Unknown	2.296	0.380
EG761851	Aryl hydrocarbon receptor 2 alpha gene; aryl hydrocarbon receptor 1 beta-like protein gene, MHC class I antigen gene, Sasa-UHA1*0101 allele, MHC class I antigen gene, Sasa-UHA2*0101 allele, and 1-acylglycerol-3-phosphate O-acyltransferase 3 gene, and pyroxidal kinase gene, partial cds [FJ969489; *Salmo salar*] (N)	218 (92%)	2e-78	Cellular Component: MHC class I protein complex (GO:0042612) [D0QYP6]	2.285	0.399
CA056588	Potential DNA-binding protein C17orf49 homolog putative mRNA [BT045676; *Salmo salar*] (N)	459 (99%)	0	DNA binding (GO:0003677) [B5X3Q7]	2.281	0.376
CA056391	Onmycontig mRNA sequence [EZ861227; *Oncorhynchus mykiss*] (N)	129 (94%)	3e-42	Unknown	2.275	0.222
CA053162	Onmycontig mRNA sequence [EZ860285; *Oncorhynchus mykiss*] (N)	129 (95%)	3e-47	Unknown	2.269	0.326
DY730158	Onmycontig mRNA sequence [EZ912532; *Oncorhynchus mykiss*] (N)	480 (95%)	0	Unknown	2.269	0.157
CX027085	Ubiquitin-protein ligase RNF8 putative mRNA [BT059506; *Salmo salar*] (N)	192 (94%)	2e-73	Ligase activity; protein binding; zinc ion binding (GO:0016874; GO:0005515; GO:0008270) [C0HB00]	2.268	0.333
DW553666	Onmycontig mRNA sequence [EZ863492; *Oncorhynchus mykiss*] (N)	447 (85%)	1e-105	Unknown	2.253	0.217
DY731837	Onmycontig mRNA sequence [EZ769153; *Oncorhynchus mykiss*] (N)	464 (86%)	1e-126	Unknown	2.250	0.098
CB506690	Unnamed protein product [CAG02378; *Tetraodon nigroviridis*]	67 (48%)	2e-10	Serine-type endopeptidase activity (GO:0004252) [Q4SAF4]	2.244	0.256
EG869972	Onmycontig mRNA sequence [EZ792040; *Oncorhynchus mykiss*] (N)	664 (88%)	0	Unknown	2.221	0.338
CA062686	Onmycontig mRNA sequence [EZ804766; *Oncorhynchus mykiss*] (N)	117 (94%)	3e-38	Unknown	2.219	0.105
CA037541	Tpr protein [AAI34978; *Danio rerio*]	142 (58%)	1e-36	Unknown [A4QN67]	2.214	0.406

CB499427	Cytokine receptor common gamma chain [AJ276623; *Oncorhynchus mykiss*] (N)	733 (90%)	0	Receptor activity (GO:0004872) [Q9DEQ1]	2.213	0.192
CA047685	Interferon-inducible GTPase_b and interferon-inducible GTPase_a genes [EU221179; *Salmo salar*] (N)	214 (98%)	9e-98	GTP binding; hydrolase activity, acting on acid anhydrides (GO:0005525; GO:0016817) [A8WCJ8]	2.208	0.447
CA060810	Probable E3 ubiquitin-protein ligase TRIP12 putative mRNA [BT072452; *Salmo salar*] (N)	642 (99%)	0	Unknown	2.190	0.283
CA053224	Immunoglobulin heavy chain gene locus [DQ400445; *Ictalurus punctatus*] (N)			Unknown [Q1WCB6]	2.189	0.069
EG935515	Phosphatidylinositol 4-kinase, catalytic, beta (predicted) [ACC64591; *Rhinolophus ferrumequinum*]	274 (91%)	9e-145	1-phosphatidylinositol 4-kinase activity; ATP binding (GO:0004430; GO:0005524) [B2KI64]	2.183	0.101
CB516196	Unknown			Unknown	2.176	0.273
DW581572	Onmycontig mRNA sequence [EZ842642; *Oncorhynchus mykiss*] (N)	370 (94%)	3e-152	Unknown	2.176	0.441
CK990511	Monocyte to macrophage differentiation protein putative mRNA [BT045655; *Salmo salar*] (N)	427 (95%)	0	Cellular Component: integral to membrane (GO:0016021) [B5X3N6]	2.168	0.321
CX357588	RAB14, member RAS oncogene family, isoform CRA_a [EDL08644; *Mus musculus*]	62 (99%)	5e-28	Unknown	2.166	0.108
DY737189	Clone BAC CHORI214-68O19 genomic sequence [GQ505860; *Salmo salar*] (N)	126 (95%)	2e-44	Receptor binding (GO:0005102) [D0UGD8]	2.160	0.129
CA046109	Onmycontig mRNA sequence [EZ905198; *Oncorhynchus mykiss*] (N)	520 (90%)	0	Unknown	2.159	0.126
CB507637	Clone BAC CHORI214-92I04 [EF427384; *Salmo salar*] (N)	238 (93%)	8e-84	Threonine-type endopeptidase activity (GO:0004298) [A7KE01]	2.149	0.176
CB499556	GTP-binding protein era homolog [ACI33449; *Salmo salar*]	114 (100%)	4e-59	GTP binding; RNA binding (GO:0005525; GO:0003723) [B5X2B8]	2.144	0.169

DY697666	Onmycontig mRNA sequence [EZ858346; *Oncorhynchus mykiss*] (N)	322 (91%)	2e-115	Unknown	2.124	0.130
CA043774	Tetratricopeptide repeat protein 32 [ACI67454; *Salmo salar*]	38 (100%)	9e-14	Unknown [B5X9D4]	2.123	0.124
CB515474	Mitochondrial import inner membrane translocase subunit Tim22 putative mRNA [BT046942; *Salmo salar*] (N)	649 (99%)	0	Protein transporter activity (GO:0008565) [B5X7C3]	2.101	0.102
CA050348	Tetraspanin-3 putative mRNA [BT071955; *Salmo salar*] (N)	501 (100%)	0	Unknown	2.092	0.212
DY694875	Clone BAC CHORI214-129P21 genomic sequence [GQ505858; *Salmo salar*] (N)	143 (93%)	3e-48	RNA binding; structural constituent of ribosome (GO:0003723; GO:0003735) [A7KIL2]	2.087	0.284
DY731539	Onmycontig mRNA sequence [EZ851708; *Oncorhynchus mykiss*] (N)	176 (95%)	8e-69	Unknown	2.077	0.289
CB511319	Onmycontig mRNA sequence [EZ912330; *Oncorhynchus mykiss*] (N)	497 (92%)	0	Unknown	2.076	0.353
CB512663	Unnamed protein product [CAF89010; *Tetraodon nigroviridis*]	80 (37%)	8e-07	Transferase activity, transferring glycosyl groups (GO:0016757) [Q4TDM2]	2.065	0.232
CA041246	C-C motif chemokine 21 precursor putative mRNA [BT048856; *Salmo salar*] (N)	699 (99%)	0	Chemokine activity (GO:0008009) [B5XCT7]	2.063	0.258
CB517439	Junction plakoglobin [ACI33223; *Salmo salar*]	201 (81%)	2e-82	Binding (GO:0005488) [B5X1P2]	2.062	0.170
CA369659	Unnamed protein product [BAG52002; *Homo sapiens*]	234 (70%)	2e-76	Rab GTPase activator activity; calcium ion binding (GO:0005097; GO:0005509) [B3KQE0]	2.057	0.277
CA050767	Onmycontig mRNA sequence [EZ911859; *Oncorhynchus mykiss*] (N)	802 (90%)	0	Unknown	2.047	0.295
CK990709	Diamine acetyltransferase 1 [ACN10066; *Salmo salar*]	79 (98%)	2e-35	N-acetyltransferase activity (GO:0008080) [C0H7P7]	2.010	0.119
CX141080	Onmycontig mRNA sequence [EZ789840; *Oncorhynchus mykiss*] (N)	411 (98%)	0	Unknown	2.005	0.313
EG842253	Churchill protein [ACI70031; *Salmo salar*]	112 (100%)	9e-64	Transcription activator activity; zinc ion binding (GO:0016563;	1.999	0.121

				GO:0008270) [B5XGR1]		
DW547488	Onmycontig mRNA sequence [EZ847641; *Oncorhynchus mykiss*] (N)	338 (89%)	3e-107	Unknown	1.992	0.254

See Appendix II for footnotes.

APPENDIX XII. Transcripts (444) with greater than 2-fold expression in triploid growth hormone transgenic Atlantic salmon family AS29 in comparison to its diploid counterparts in any 3 out of 4 technical replicated arrays.

EST	Gene Name of Best BLASTX or BLASTN (N) Hit	Length (% ID)	E value	Function of Best BLASTX Hit	$\bar{X}$ Fold Change	SE
DW584490	Heat shock 70 kDa protein [ACI34374; *Salmo salar*]	126 (99%)	3e-66	ATP binding (GO:0005524) [B5X4Z3]	49.345	25.409
CB509791	Zgc: 113828 [AAH96945; *Danio rerio*]	119 (53%)	2e-24	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q4V9D6]	36.246	21.281
CB493880	FK506-binding protein 1A [ACO08345; *Oncorhynchus mykiss*]	29 (100%)	5e-18	Peptidyl-prolyl cis-trans isomerase activity (GO:0003755) [C1BH42]	26.652	24.451
CK991176	Alpha-enolase putative mRNA [BT072686; *Salmo salar*] (N)	150 (99%)	6e-68	Unknown	26.456	24.216
CK991274	Annexin A4 [ACI69256; *Salmo salar*]	106 (98%)	9e-51	Calcium ion binding; calcium-dependent phospholipid binding (GO:0005509; GO:0005544) [B5XEI6]	22.321	18.356
CA052791	Onmycontig mRNA sequence [EZ846431; *Oncorhynchus mykiss*] (N)	286 (91%)	6e-98	Unknown	21.996	19.012
CB485951	HSC71 [AAB21658; *Oncorhynchus mykiss*]	182 (100%)	5e-99	ATP binding (GO:0005524) [P08108]	21.329	4.206
CB496971	Apolipoprotein A-I-2 [AAB96973; *Oncorhynchus mykiss*]	54 (100%)	1e-13	Lipid binding (GO:0008289) [O57524]	20.689	6.493
CA041892	Apolipoprotein A-I precursor [ACI68193; *Salmo salar*]	44 (100%)	5e-16	Lipid binding (GO:0008289) [B5XBH3]	20.559	4.665
CA038814	Reverse transcriptase [AAS83200; *Fundulus heteroclitus*]	115 (29%)	1e-08	RNA binding; RNA-directed DNA polymerase activity (GO:0003723; GO:0003964) [Q64IX6]	18.689	2.176
CB492746	Cyp2x [ACO35044; *Larimichthys crocea*]	110 (74%)	3e-44	Electron carrier activity ; heme binding; monooxygenase	15.816	11.591

				activity (GO:0009055; GO:0020037; GO:0004497) [C1K735]		
CB500378	Interferon-induced guanylate-binding protein 1 putative mRNA [BT058872; *Salmo salar*] (N)	651 (100%)	0	GTP binding; GTPase activity (GO:0005525; GO:0003924) [C0H966]	15.687	9.290
CB496584	Alpha actin [AAF75784|AF267496; *Salmo trutta*]	112 (99%)	1e-58	ATP binding; protein binding (GO:0005524; GO:0005515) [Q9I8K1]	15.251	9.945
CA041940	Elongation factor EF1 alpha [ACP56687; *Oncorhynchus tshawytscha*]	45 (100%)	4e-17	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C3VPX4]	15.216	5.224
CA042402	Apolipoprotein B [ADG29181; *Epinephelus coioides*]	36 (56%)	5e-05	Unknown [D6PVT6]	14.188	8.845
CB496919	Glycerol-3-phosphate dehydrogenase [AAK07737; *Salmo salar*]	36 (98%)	8e-14	NAD or NADH binding; glycerol-3-phosphate dehydrogenase [NAD+] activity; protein homodimerization activity (GO:0051287; GO:0004367; GO:0042803) [Q98SJ9]	11.899	5.595
CA045526	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial precursor [ACI69573; *Salmo salar*]	26 (100%)	1e-05	Iron ion binding; iron-sulfur cluster binding; protein binding (GO:0005506; GO:0051536; GO:0005515) [B5XFF3]	11.363	6.086
CA057197	NudC domain-containing protein 3 putative mRNA [BT072335; *Salmo salar*] (N)	636 (99%)	0	Unknown	11.101	5.640
CA056648	Onmycontig mRNA sequence [EZ887914; *Oncorhynchus mykiss*] (N)	326 (84%)	3e-76	Unknown	10.750	6.957
CA038301	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*]	76 (90%)	4e-30	Unknown [Q8JJ66]	10.226	2.293
CA055438	BarH-like 2 homeobox protein-like [DAA31425; *Bos taurus*]	129 (94%)	1e-60	Unknown	10.024	4.870
CB488923	Glycine cleavage system H protein,	60 (97%)	3e-25	Cellular component: glycine	9.708	4.011

	mitochondrial precursor [ACN10330; *Salmo salar*]			cleavage complex; mitochondrion (GO:0005960; GO:0005739) [C0H8G1]		
CB492813	Glyceraldehyde-3-phosphate dehydrogenase [ACI33883; *Salmo salar*]	113 (100%)	7e-54	NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X3K2]	9.559	4.234
CA060826	Elongation factor 1-alpha 1 [ACN11490; *Salmo salar*]	38 (100%)	2e-11	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	9.211	1.348
CB493595	Delta5-desaturase-like protein [ABU87822; *Oncorhynchus masou*]	87 (99%)	2e-45	heme binding; oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [A7XUS7]	9.210	4.620
CA050955	RNA-binding protein PNO1 [ACO13732; *Esox lucius*]	106 (99%)	4e-51	RNA binding (GO:0003723) [C1BXH9]	8.806	4.187
CB494013	Onmycontig mRNA sequence [EZ908260; *Oncorhynchus mykiss*] (N)	585 (99%)	0	Unknown	8.801	4.509
CK991311	Onmycontig mRNA sequence [EZ908637; *Oncorhynchus mykiss*] (N)	353 (94%)	1e-144	Unknown	8.628	3.992
CB488137	High mobility group-T protein [ACN11467; *Salmo salar*]	156 (99%)	1e-86	DNA binding; transposase activity (GO:0003677; GO:0004803) [C0HBP8]	8.582	4.843
CB492565	Si: dkey-14d8.7 protein [AAI35062; *Danio rerio*]	174 (59%)	6e-62	Unknown [A4QN85]	8.496	2.623
CB499596	Hydroxysteroid dehydrogenase-like protein 2 [ACN10404; *Salmo salar*]	103 (100%)	7e-40	Oxidoreductase activity; sterol binding (GO:0016491; GO:0032934) [C0H8N5]	8.428	5.662
EG925336	HCG40021 [EAW75736; *Homo*	83 (47%)	6e-17	Unknown	8.416	1.809

	sapiens]					
CB493973	Apolipoprotein B [CAA57449; *Salmo salar*]	60 (74%)	2e-08	Unknown [Q91480]	8.051	3.549
CB514092	Glutamine synthetase [ACI68482; *Salmo salar*]	27 (100%)	4e-08	Glutamate-ammonia ligase activity (GO:0004356) [B5XCB2]	7.449	2.855
CB498324	Elongation factor 1-alpha [ACN10642; *Salmo salar*]	145 (100%)	1e-77	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	7.195	0.441
CB517817	Glutamine synthetase [ACI68482; *Salmo salar*]	99 (100%)	6e-52	Glutamate-ammonia ligase activity (GO:0004356) [B5XCB2]	7.174	2.305
CB496520	Cytochrome P450 [AAD54014; *Fundulus heteroclitus*]	110 (70%)	3e-61	Electron carrier activity; heme binding; monooxygenase activity (GO:0009055; GO:0020037; GO:0004497) [Q9PVI1]	7.143	1.188
CB486904	40S ribosomal protein S3 [ACI67079; *Salmo salar*]	137 (100%)	2e-70	RNA binding; structural constituent of ribosome (GO:0003723; GO:0003735) [B5X8A9]	6.978	0.681
EG910863	Serum albumin 2 [CAA43187; *Salmo salar*]	232 (79%)	1e-96	Lipid binding; metal ion binding (GO:0008289; GO:0046872) [Q03156]	6.904	0.851
CA055480	Unknown				6.842	2.037
CA060746	Heme oxygenase [ACI67681; *Salmo salar*]	131 (94%)	2e-52	Heme oxygenase (decyclizing) activity (GO:0004392) [B5XA11]	6.821	2.258
CB510212	Ribosomal protein S5 [BAF45893; *Solea senegalensis*]	86 (98%)	1e-41	RNA binding; structural constituent of ribosome (GO:0003723; GO:0003735) [A2Q0S0]	6.813	1.315
CA043736	Elongation factor 2 [ACN58670; *Salmo salar*]	211 (100%)	2e-119	GTP binding; translation elongation factor activity (GO:0005525; GO:0003746)	6.664	2.306

				[C0PUE5]		
DY732008	Heat shock protein HSP 90-alpha [ACN10985; *Salmo salar*]	173 (99%)	7e-80	ATP binding; unfolded protein binding (GO:0005524; GO:0051082) [C0HAB6]	6.663	2.420
CA056664	Elongation factor 1-delta [ACI69759; *Salmo salar*]	163 (100%)	2e-74	Translation elongation factor activity (GO:0003746) [B5XFY9]	6.548	1.691
CB496788	Glutathione S-transferase A [ACO07597; *Oncorhynchus mykiss*]	101 (100%)	3e-53	Transferase activity (GO:0016740) [C1BEZ4]	6.484	1.274
CA044104	Selenoprotein Pa precursor putative mRNA [BT072678; *Salmo salar*] (N)	684 (99%)	0	Unknown	6.481	0.417
CB494346	Enolase 3-1 [ACH70930; *Salmo salar*]	182 (99%)	2e-101	Magnesium ion binding; phosphopyruvate hydratase activity (GO:0000287; GO:0004634) [B5DGQ6]	6.475	2.304
CB498391	Beta-2 microgloblin [AAB04653; *Oncorhynchus mykiss*]	116 (100%)	4e-62	Cellular Component: MHC class I protein complex (GO:0042612) [Q91966]	6.426	3.892
CB503997	Eukaryotic translation initiation factor 5A-1 [ACM08851; *Salmo salar*]	109 (100%)	1e-56	RNA binding; ribosome binding; translation elongation factor activity; translation initiation factor activity (GO:0003723; GO:0043022; GO:0003746; GO:0003743) [B9EMV4]	6.279	3.587
CK991342	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*]	50 (84%)	4e-19	Unknown [Q8JJ66]	6.277	0.724
CA051690	Coiled-coil transcriptional coactivator b, homeobox protein HoxC13bb, homeobox protein HoxC12bb, and homeobox protein HoxC11bb genes, complete cds; HoxC10bb pseudogene, partial sequence; and homeobox protein HoxC9bb, homeobox protein HoxC8bb, homeobox protein HoxC6bb, homeobox protein HoxC5bb, homeobox protein HoxC4bb, and single-strand selective	317 (95%)	2e-134	Sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity (GO:0043565; GO:0003700) [B3SU99]	6.197	2.691

	monofunctional uracil genes, complete cds [EU025717; *Salmo salar*] (N)					
CK990607	Complement C1q-like protein 4 precursor [ACM09542; *Salmo salar*]	101 (46%)	2e-18	Unknown [B9EPU5]	6.027	0.755
CB501366	Unnamed protein product [CAG02807; *Tetraodon nigroviridis*]	123 (62%)	6e-37	Channel activity (GO:0015267) [Q4S975]	5.938	1.818
CA040124	Selenoprotein Pa precursor putative mRNA [BT072678; *Salmo salar*] (N)	730 (99%)	0	Unknown	5.892	1.389
CA043324	Beta-2-microglobulin precursor putative mRNA [BT047559; *Salmo sala*] (N)	542 (99%)	0	Cellular Component: MHC class I protein complex (GO:0042612) [Q9DD81]	5.811	1.521
CA043764	Glycine cleavage system H protein, mitochondrial precursor [ACN10330; *Salmo salar*]	79 (100%)	4e-38	Glycine cleavage complex; mitochondrion (GO:0005960; GO:0005739) [C0H8G1]	5.808	1.117
CB504246	FBP32II precursor [ABB29992; *Morone chrysops*]	153 (68%)	7e-51	Biological Process: cell adhesion (GO:0007155) [Q2LK87]	5.800	2.822
CA064237	Onmycontig mRNA sequence [EZ784403; *Oncorhynchus mykiss*] (N)	728 (95%)		Unknown	5.739	1.397
EG802027	Heat shock protein hsp90 [AAB49983; *Oncorhynchus tshawytscha*]	157 (82%)	2e-39	ATP binding; unfolded protein binding (GO:0005524; GO:0051082) [P87397]	5.712	2.296
CB490824	Notchless protein homolog 1 [ACN58698; *Salmo salar*]	67 (100%)	5e-33	Unknown [C0PUL3]	5.662	1.647
CA769454	Selenoprotein Pa precursor putative mRNA [BT072678; *Salmo salar*] (N)	706 (100%)	0	Unknown	5.659	1.827
CB505764	Complement C1q-like protein 4 precursor [ACM09542; *Salmo salar*]	117 (48%)	2e-25	Unknown [B9EPU5]	5.639	0.642
CB494727	Onmycontig mRNA sequence [EZ767124; *Oncorhynchus mykiss*] (N)	491 (100%)	0	Unknown	5.632	1.412
CB509189	Alpha actin [AAF75784|AF267496; *Salmo trutta*]	137 (100%)	4e-75	ATP binding; protein binding (GO:0005524; GO:0005515) [Q9I8K1]	5.609	2.048
CB503548	Sec61 alpha form A-like mRNA [BT044020; *Salmo salar*] (N)	688 (99%)	0	P-P-bond-hydrolysis-driven protein transmembrane transporter activity (GO:0015450) [B5RI96]	5.508	1.109
CB498328	Eukaryotic translation elongation factor	47 (92%)	5e-18	GTP binding; GTPase activity;	5.473	1.651

	2 [ABK58358; *Callithrix jacchus*]			translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [A0SXL6]		
CB494453	Onmycontig mRNA sequence [EZ906468; *Oncorhynchus mykiss*] (N)	411 (91%)	1e-146	Unknown	5.441	1.798
CB497097	Complement factor H1 protein [ABY55261; *Oncorhynchus masou formosanus*]	117 (86%)	4e-56	Unknown [B0FFJ7]	5.412	0.715
CA040843	Epithelial cadherin precursor [ACN10577; *Salmo salar*]	213 (98%)	4e-108	Calcium ion binding (GO:0005509) [C0H958]	5.407	2.014
CA061181	Onmycontig mRNA sequence [EZ793168; *Oncorhynchus mykiss*] (N)	700 (96%)	0	Unknown	5.394	2.964
CB494095	Superoxide dismutase putative mRNA [BT073392; *Oncorhynchus mykiss]* (N)	534 (98%)	0	Metal ion binding; superoxide dismutase activity (GO:0046872; GO:0004784) [C1BFL3]	5.357	0.612
CA053189	Glutamate dehydrogenase 1, mitochondrial precursor putative mRNA [BT044837; *Salmo salar*] (N)	515 (100%)	0	Binding; oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor (GO:0005488; GO:0016639) [B5X1B8]	5.290	0.973
CB509933	Complement factor H precursor [CAF25505; *Oncorhynchus mykiss*]	137 (76%)	6e-56	Unknown [Q2L4Q6]	5.275	0.616
CA061175	Cytochrome P450 [AAC98961; *Dicentrarchus labrax*]	87 (81%)	4e-34	Electron carrier activity; heme binding; monooxygenase activity (GO:0009055; GO:0020037; GO:0004497) [Q9YI34]	5.263	2.015
CB499364	Transport protein Sec61 subunit alpha isoform A [ACI33703; *Salmo salar*]	193 (99%)	2e-103	P-P-bond-hydrolysis-driven protein transmembrane transporter activity (GO:0015450) [B5X322]	5.235	1.033
CB492852	C-type MBL-2 protein [CAJ14130; *Oncorhynchus mykiss*]	145 (100%)	1e-97	Sugar binding (GO:0005529) [Q4LAN6]	5.168	1.622
CA061418	Onmycontig mRNA sequence [EZ829065; *Oncorhynchus mykiss*] (N)	530 (80%)	4e-71	Unknown	5.168	0.875

CA060068	Disulfide-isomerase A3 precursor [ACI34304; *Salmo salar*]	112 (100%)	2e-61	Isomerase activity (GO:0016853) [B5X4S3]	5.168	2.507
DY724422	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform putative mRNA [BT044851; *Salmo salar*] (N)	681 (99%)	0	Phosphoprotein phosphatase activity (GO:0004721) [B5X1D2]	5.069	1.413
CA043777	Onmycontig mRNA sequence [EZ861225; *Oncorhynchus mykiss*] (N)	221 (94%)	7e-84	Unknown	5.044	0.605
CA038719	Complement component C3 [AAB05029; *Oncorhynchus mykiss*]	101 (92%)	3e-46	Endopeptidase inhibitor activity; protein binding (GO:0004866; GO:0005515) [P98093]	5.036	1.913
CB515442	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase [AAP36549; *Synthetic construct*]	193 (100%)	2e-106	Unknown	5.022	1.306
CA063531	Cold-inducible RNA-binding protein putative mRNA [BT058753; *Salmo salar*] (N)	627 (99%)	0	Nucleic acid binding; nucleotide binding (GO:0003676; GO:0000166) [C0H8U7]	4.989	0.962
CA044829	Onmycontig mRNA sequence [EZ771918; *Oncorhynchus mykiss*] (N)	359 (84%)	1e-81	Unknown	4.963	0.911
CB502683	HSC71 [AAB21658; *Oncorhynchus mykiss*]	212 (100%)	7e-95	ATP binding (GO:0005524)[P08108]	4.911	1.442
CK990940	Unknown				4.851	0.557
CA056224	Clone ssal-rgf-540-084 [BT072779; *Salmo salar*] (N)	655 (100%)	0	Unknown	4.833	1.800
CB499769	Cold-inducible RNA-binding protein [ACM09312; *Salmo salar*]	28 (100%)	4e-07	Nucleic acid binding; nucleotide binding (GO:0003676; GO:0000166) [B9EP65]	4.792	1.137
CB494587	Glutathione peroxidase type 2 [AAV32968; *Oncorhynchus mykiss*]	71 (85%)	4e-28	Glutathione peroxidase activity (GO:0004602) [Q5UTE7]	4.744	1.898
CB493926	K18, simple type I keratin [CAA74664; *Oncorhynchus mykiss*]	73 (100%)	6e-24	Structural molecule activity (GO:0005198) [O57607]	4.646	1.328
DY733552	Elongation factor 1-alpha 1 putative mRNA [BT059777; *Salmo salar*] (N)	628 (100%)	0	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0HBS1]	4.600	0.630
CB505935	Selenoprotein Pa precursor putative mRNA [BT072678; *Salmo salar*] (N)	511 (100%)	0	Unknown	4.573	0.736

EG793488	Membrane-spanning 4-domains subfamily A member 4A [ACI69003; *Salmo salar*]	200 (79%)	1e-70	Cellular Component: integral to membrane (GO:0016021) [B5XDT3]	4.522	0.938
CK991349	Onmycontig mRNA sequence [EZ782390; *Oncorhynchus mykiss*] (N)	465 (99%)	0	Unknown	4.517	0.383
EG795851	Troponin T, slow skeletal muscle [ACM09392; *Salmo salar*]	190 (100%)	9e-92	Unknown [B9EPE5]	4.512	0.995
CB492405	40S ribosomal protein S11 [ACO15454; *Caligus clemensi*]	105 (100%)	1e-53	Structural constituent of ribosome (GO:0003735) [C1C2F1]	4.485	0.417
CB498222	Actin [AAK60616|AF330142; *Oncorhynchus mykiss*]	78 (100%)	2e-37	ATP binding; protein binding (GO:0005524; GO:0005515) [Q90WC5]	4.423	1.182
CB511435	Complement factor Bf-1 [AAC83699; *Oncorhynchus mykiss gairdneri*]	151 (76%)	4e-62	Serine-type endopeptidase activity (GO:0004252) [Q9YGE7]	4.401	0.923
DY711246	Onmycontig mRNA sequence [EZ764913; *Oncorhynchus mykiss*] (N)	559 (95%)	0	Unknown	4.379	0.623
CA063468	Lysosomal-associated transmembrane protein 4A putative mRNA [BT045705; *Salmo salar*] (N)	578 (100%)	0	Cellular Component: integral to membrane (GO:0016021) [B5X3T6]	4.367	2.017
CA061048	Beta-2-microglobulin precursor putative mRNA [BT047559; *Salmo salar*] (N)	608 (99%)	0	Cellular Component: MHC class I protein complex (GO:0042612) [Q9DD81]	4.345	0.976
CA369135	C type lectin receptor C [AAT77222; *Salmo salar*]	186 (94%)	1e-76	Receptor activity; sugar binding (GO:0004872; GO:0005529)[Q68S96]	4.334	0.692
CB492705	Mitochondrial complex I subunit NDUFB2 [ACL68409; *Oncorhynchus mykiss*]	52 (100%)	6e-27	Unknown [B8YI11]	4.310	1.562
CB511022	Glyceraldehyde-3-phosphate dehydrogenase [ACI33883; *Salmo salar*]	112 (100%)	3e-53	NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X3K2]	4.309	1.266
BU965756	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo*	116 (100%)	3e-60	NAD or NADH binding; glyceraldehyde-3-phosphate	4.299	0.788

	salar]			dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]		
CB509521	Beta-2-glycoprotein 1 precursor [ACN10110; *Salmo salar*]	211 (84%)	2e-110	Unknown [C0H7U1]	4.288	0.798
CK990215	Onmycontig mRNA sequence [EZ764509; *Oncorhynchus mykiss*] (N)	213 (93%)	5e-80	Unknown	4.271	0.344
CK990337	Mitochondrial import receptor subunit TOM7 homolog putative mRNA [BT048608; *Salmo salar*] (N)	387 (96%)	3e-171	P-P-bond-hydrolysis-driven protein transmembrane transporter activity; receptor activity (GO:0015450; GO:0004872) [B5X7Q4]	4.232	0.693
CB494476	S-adenosylhomocysteine hydrolase [ACH70814; *Salmo salar*]	185 (99%)	1e-102	Adenosylhomocysteinase activity; binding (GO:0004013; GO:0005488) [B5DGE0]	4.232	0.662
CK990802	NACHT, LRR and PYD domains-containing protein 1 putative mRNA [BT072692; *Salmo salar*] (N)	188 (85%)	8e-38	Unknown	4.219	2.406
CK990274	Unknown				4.202	0.954
DW564611	Unnamed protein product [CAF95001; *Tetraodon nigroviridis*]	94 (94%)	1e-40	Unknown [Q4SWI1]	4.192	0.932
CB514428	Onmycontig mRNA sequence [EZ908375; *Oncorhynchus mykiss*] (N)	760 (92%)	0	Unknown	4.164	1.320
CB494398	Disulfide-isomerase A3 precursor [ACI34304; *Salmo salar*]	46 (94%)	1e-15	Isomerase activity (GO:0016853) [B5X4S3]	4.134	0.942
CB498772	Eif4a1b protein [AAI53508; *Danio rerio*]	189 (92%)	2e-92	ATP binding; ATP-dependent helicase activity; nucleic acid binding (GO:0005524; GO:0008026; GO:0003676) [A8E590]	4.132	1.024
CA062835	Cold-inducible RNA-binding protein [ACN10466; *Salmo salar*]	83 (99%)	2e-39	Nucleic acid binding; nucleotide binding (GO:0003676; GO:0000166) [C0H8U7]	4.124	0.635
CB497394	Beta-2 microglobulin mRNA [L63533|ONHB2MD *Oncorhynchus mykiss*] (N)	505 (93%)	0	Cellular Component: MHC class I protein complex (GO:0042612) [Q91202]	4.118	0.645

CB493785	Complement factor H1 protein [ABY55261; *Oncorhynchus masou formosanus*]	149 (82%)	1e-69	Unknown [B0FFJ7]	4.113	0.491
CB498361	Glyceraldehyde-3-phosphate dehydrogenase [ACI66269; *Salmo salar*]	146 (99%)	6e-78	NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5X5Z9]	4.105	0.829
CB510407	Cytochrome P450 3A27 [ACI33861; *Salmo salar*]	205 (100%)	3e-115	Electron carrier activity; heme binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen (GO:0009055; GO:0020037; GO:0016712) [B5X3I0]	4.104	1.378
CB505897	Beta-2 microglobulin type 2 [AAP51056; *Oncorhynchus mykiss*]	24 (92%)	1e-12	Cellular Component: MHC class I protein complex (GO:0042612) [Q6XQ10]	4.081	0.498
CB492394	Elongation factor 1-alpha [ACN10642; *Salmo salar*]	148 (100%)	2e-79	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	4.068	0.483
CB496932	Fructose-1, 6-bisphosphatase [ACH70893; *Salmo salar*]	190 (97%)	1e-119	Fructose 1,6-bisphosphate 1-phosphatase activity (GO:0042132) [B5DGL9]	4.041	1.535
CB493939	Onmycontig mRNA sequence [EZ763719; *Oncorhynchus mykiss*] (N)	646 (97%)	0	Unknown	3.987	1.652
CB493178	Ferritin-H subunit [AAK08117|AF338763; *Oncorhynchus nerka*]	65 (96%)	6e-57	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [Q98TT0]	3.972	0.540
CA366949	Onmycontig mRNA sequence	542 (99%)	0	Unknown	3.968	0.578

	[EZ894249; *Oncorhynchus mykiss*] (N)					
CA058039	Kininogen-1 precursor [ACO13619; *Esox lucius*]	181 (62%)	5e-52	Cysteine-type endopeptidase inhibitor activity (GO:0004869) [C1BX66]	3.950	0.662
CB509563	Onmycontig mRNA sequence [EZ871571; *Oncorhynchus mykiss*] (N)	513 (89%)	3e-161	Unknown	3.932	0.550
CA054111	Gamma-aminobutyric acid receptor-associated protein-like 2 [ACI66147; *Salmo salar*]	78 (100%)	7e-37	Receptor activity (GO:0004872) [B5X5M7]	3.919	1.214
EG835892	Zinc finger protein 180 (HHZ168), isoform CRA_d [EAW57277; *Homo sapiens*]	273 (58%)	1e-84	Unknown	3.909	0.506
CB490426	Ubiquitin-conjugating enzyme E2 T [ACM09373; *Salmo salar*]	133 (99%)	2e-71	Small conjugating protein ligase activity (GO:0019787) [B9EPC6]	3.908	0.597
CB497299	Elongation factor 1-beta [ACI68836; *Salmo salar*]	164 (97%)	2e-64	Translation elongation factor activity (GO:0003746) [B5XDB6]	3.883	0.845
CK991317	Onmycontig mRNA sequence [EZ764925; *Oncorhynchus mykiss*] (N)	377 (95%)	2e-164	Unknown	3.854	0.806
CA050185	Calmodulin 2 [AAX37095; *Synthetic construct*]	143 (96%)	3e-71	Unknown	3.834	1.338
CA043745	Lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog [ACI67970; *Salmo salar*]	151 (99%)	1e-61	Unknown [B5XAV0]	3.832	0.825
CK990806	Beta-2-microglobulin precursor putative mRNA [BT056667; *Salmo salar*] (N)	165 (99%)	2e-74	Cellular Component: MHC class I protein complex (GO:0042612) [B9ELZ2]	3.806	1.202
CA055482	RCG61927 [EDM02821; *Rattus norvegicus*]	70 (43%)	5e-08	Unknown	3.783	0.808
CB491051	60S ribosomal protein L10a [ACO08534; *Oncorhynchus mykiss*]	179 (99%)	2e-83	RNA binding; structural constituent of ribosome (GO:0003723; GO:0003735) [C1BHN1]	3.776	0.459
CA062591	Cold-inducible RNA-binding protein putative mRNA [BT056773; *Salmo salar*] (N)	516 (99%)	0	Nucleic acid binding; nucleotide binding (GO:0003676; GO:0000166) [B5DGC5]	3.753	1.427

CB492435	Onmycontig mRNA sequence [EZ765170; *Oncorhynchus mykiss*] (N)	636 (99%)	0	Unknown	3.752	0.515
CB516919	Extracellular matrix protein 1 precursor [ACN10906; *Salmo salar*]	97 (97%)	1e-48	Cellular Component: extracellular space (GO:0005615) [C0HA37]	3.743	0.757
CB494344	Actin [AAK60616|AF330142; *Oncorhynchus mykiss*]	102 (100%)	6e-53	ATP binding; protein binding (GO:0005524; GO:0005515) [Q90WC5]	3.702	1.310
CB489257	Ferritin heavy subunit [AAB34575; *Salmo salar*]	139 (99%)	9e-77	Ferric iron binding; ferroxidase activity (GO:0008199; GO:0004322) [P49946]	3.691	0.777
CB503169	Fish-egg lectin [ACM09206; *Salmo salar*]	84 (100%)	4e-44	Sugar binding (GO:0005529) [B9ENV9]	3.672	0.864
CA054079	Retinol dehydrogenase 3 [ACI67927; *Salmo salar*]	191 (92%)	1e-98	Oxidoreductase activity (GO:0016491) [B5XAQ7]	3.670	0.766
CB509722	Glutathione peroxidase 3 precursor putative mRNA [BT072794; *Salmo salar*] (N)	492 (99%)	0	Unknown	3.664	0.488
CB498098	Elongation factor EF1 alpha [ACP56687; *Oncorhynchus tshawytscha*]	64 (99%)	1e-27	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C3VPX4]	3.656	0.724
EG792456	Succinate dehydrogenase iron-sulfur protein, mitochondrial precursor [ACO07425; *Oncorhynchus mykiss*]	240 (99%)	1e-141	Electron carrier activity; iron-sulfur cluster binding; oxidoreductase activity (GO:0009055; GO:0051536; GO:0016491) [C1BEH2]	3.635	1.108
CB516126	Translocon-associated protein subunit delta precursor putative mRNA [BT057917; *Salmo salar*] (N)	701 (100%)	0	Cellular Component: endoplasmic reticulum; integral to membrane (GO:0005783; GO:0016021) [B9EQJ2]	3.632	1.175
CB509813	Lectin precursor [ACN09984; *Salmo salar*]	75 (46%)	4e-11	Sugar binding (GO:0005529) [C0H7G5]	3.605	0.928
CB492616	Unnamed protein product [CAG05386; *Tetraodon nigroviridis*]	186 (95%)	6e-110	Unknown [Q4S1U6]	3.599	1.133
CB498050	Onmycontig mRNA sequence [EZ764794; *Oncorhynchus mykiss*] (N)	644 (99%)	0	Unknown	3.588	1.014

EG936494	78 kDa glucose-regulated protein precursor [ACI33778; *Salmo salar*]	197 (99%)	2e-106	ATP binding (GO:0005524) [B5X397]	3.587	0.663
CA062494	Extracellular matrix protein 1 precursor putative mRNA [BT059193; *Salmo salar*] (N)	566 (96%)	0	Cellular Component: extracellular space (GO:0005615) [C0HA37]	3.572	0.759
CA054236	40S ribosomal protein SA [ACO09157; *Osmerus mordax*]	106 (79%)	9e-37	Structural constituent of ribosome (GO:0003735) [C1BJF4]	3.561	0.675
CK990375	Onmycontig mRNA sequence [EZ764857; *Oncorhynchus mykiss*] (N)	433 (90%)	2e-144	Unknown	3.530	0.286
CA054221	Zonadhesin-like gene [AY785950; *Salmo salar*] (N)	448 (85%)	5e-110	Cellular Component: membrane (GO:0016020) [Q5S3N1]	3.486	0.748
CB516893	Hemoglobin subunit alpha-4 [ACN09908; *Salmo salar*]	71 (99%)	9e-55	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H789]	3.480	0.417
CA048856	Transposable element Tcb2 transposase [ACN10944; *Salmo salar*]	52 (89%)	2e-30	Unknown [C0HA75]	3.478	0.486
CB497796	Cystatin precursor [ACI66376; *Salmo salar*]	114 (85%)	2e-44	Cysteine-type endopeptidase inhibitor activity (GO:0004869) [B5X6A6]	3.475	0.697
CB497678	Elongation factor 1-alpha [ACN10642; *Salmo salar*]	51 (100%)	2e-20	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	3.472	0.522
CA043730	Fructose-bisphosphate aldolase B [ACN10100; *Salmo salar*]	116 (94%)	5e-49	Fructose-bisphosphate aldolase activity (GO:0004332) [C0H7T1]	3.466	0.933
CB496456	Proteasome subunit alpha type 3 [ACO07671; *Oncorhynchus mykiss*]	142 (100%)	9e-70	Threonine-type endopeptidase activity (GO:0004298) [C1BF68]	3.466	0.718
CA042698	Elongation factor 1-alpha [ACN10642; *Salmo salar*]	99 (100%)	1e-49	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9C3]	3.464	0.798
CB494413	Onmycontig mRNA sequence	706 (99%)	0	Unknown	3.460	0.479

	[EZ768185; *Oncorhynchus mykiss*] (N)					
CA049943	Adenylyl cyclase-associated protein 1 putative mRNA [BT045210; *Salmo salar*] (N)	610 (99%)	0	Actin binding (GO:000377) [B5X2E1]	3.456	1.044
CB512708	Carboxypeptidase N catalytic chain precursor [ACN10284; *Salmo salar*]	217 (100%)	7e-128	Metallocarboxypeptidase activity; zinc ion binding (GO:000418; GO:0008270) [C0H8B5]	3.446	0.543
CA041067	5-aminolevulinate synthase, erythroid-specific, mitochondrial precursor [ACN10630; *Salmo salar*]	30 (100%)	2e-10	5-aminolevulinate synthase activity; pyridoxal phosphate binding; Transferase activity, transferring nitrogenous groups (GO:0003870; GO:0030170; GO:0016769) [C0H9B1]	3.446	0.918
CB504014	28S ribosomal protein S18a, mitochondrial precursor [ACO08097; *Oncorhynchus mykiss*]	61 (100%)	4e-30	Structural constituent of ribosome (GO:0003735) [C1BGE4]	3.434	0.676
CA044554	Prothymosin alpha [ACM09466; *Salmo salar*]	111 (99%)	9e-17	Unknown [B9EPL9]	3.429	0.999
CB497136	ATP synthase subunit e, mitochondrial [ACI66375; *Salmo salar*]	71 (96%)	2e-18	Hydrogen ion transmembrane transporter activity (GO:0015078) [B5X6A5]	3.422	0.730
CB487639	Ferritin, middle subunit [ACI66713; *Salmo salar*]	130 (95%)	7e-67	Ferric iron binding (GO:0008199) [B5X793]	3.418	0.526
CB515027	Cytochrome b-c1 complex subunit 1, mitochondrial precursor [ACN58644; *Salmo salar*]	147 (100%)	1e-83	Metalloendopeptidase activity; zinc ion binding (GO:0004222; GO:0008270) [C0PUA8]	3.415	0.628
CA054202	Delta-6 fatty acyl desaturase D6fad_a gene [AY736067; *Salmo salar*] (N)	466 (96%)	0	Heme binding; oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water (GO:0020037; GO:0016717) [Q6SES0]	3.405	0.279
CB496430	Onmycontig mRNA sequence [EZ910586; *Oncorhynchus mykiss*] (N)	411 (93%)	2e-158	Unknown	3.395	0.607

CA039745	Hemoglobin subunit alpha [ACN10174; *Salmo salar*]	91 (91%)	1e-38	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C0H805]	3.389	0.705
CB510905	Brain protein 44-like protein [ACI66404; *Salmo salar*]	80 (100%)	1e-39	Unknown [B5X6D4]	3.387	0.609
CB497820	Solute carrier family 25-2 [ACH71015; *Salmo salar*]	81 (100%)	9e-40	Binding; transporter activity (GO:0005488; GO:0005215) [B5DGZ1]	3.385	0.561
CB510481	Cold-inducible RNA-binding protein putative mRNA [BT125559; *Salmo salar*] (N)	588 (99%)	0	Unknown	3.384	0.385
CB497324	Translocon-associated protein subunit beta precursor [ACO13626; *Esox lucius*]	110 (100%)	1e-57	Cellular Component: endoplasmic reticulum; integral to membrane (GO:0005783; GO:0016021) [C1BX73]	3.380	1.438
CB497954	Onmycontig mRNA sequence [EZ765170; *Oncorhynchus mykiss*] (N)	623 (99%)	0	Unknown	3.372	0.668
CB496780	Kif1-binding protein [ABW89743; *Danio rerio*]	67 (74%)	4e-10	Cellular Component: mitochondrion (GO:0005739) [A8WE67]	3.372	0.484
CA042157	Beta-2-microglobulin precursor [ACM08628; *Salmo salar*]	68 (100%)	6e-34	Cellular Component: MHC class I protein complex (GO:0042612) [B9EM81]	3.358	0.639
CK991330	Hypothetical protein PANDA_002907 [EFB16835; *Ailuropoda melanoleuca*]	31 (100%)	6e-09	Unknown [D2H0F9]	3.358	0.507
CA059282	Onmycontig mRNA sequence [EZ763644; *Oncorhynchus mykiss*] (N)	466 (93%)	8e-178	Unknown	3.355	1.461
CB497409	Onmycontig mRNA sequence [EZ785438; *Oncorhynchus mykiss*] (N)	340 (99%)	8e-173	Unknown	3.352	0.537
CK991068	Hepcidin-1 precursor [ACI67048; *Salmo salar*]	31 (94%)	5e-13	Cellular Component: extracellular region (GO:0005576) [B5X878]	3.351	0.942
CN442513	Cytochrome oxidase subunit II [AAD04736; *Salmo salar*]	226 (94%)	9e-102	Copper ion binding; cytochrome-c oxidase activity; electron carrier activity; heme binding (GO:0005507; GO:0004129;	3.338	1.009

				GO:0009055; GO:0020037) [Q37677]		
CA052576	Ribosomal protein S3-2 [ACH71009; *Salmo salar*]	180 (100%)	1e-97	RNA binding; structural constituent of ribosome (GO:0003723; GO:0003735) [B5DGY5]	3.337	0.901
CA050838	CWC15 homolog [ACM08285; *Salmo salar*]	80 (100%)	1e-33	Cellular Component: spliceosomal complex (GO:0005681) [B9EL88]	3.335	1.165
DY724400	Unknown				3.325	0.232
CB491411	Apolipoprotein C-I precursor [ACI69086; *Salmo salar*]	87 (96%)	3e-39	Cellular Component: extracellular region (GO:0005576) [B5XE16]	3.311	0.245
CB498322	Tubulin, alpha 8 like 2 [ACH70822; *Salmo salar*]	77 (99%)	7e-33	GTP binding; GTPase activity; structural molecule activity (GO:0005525; GO:0003924; GO:0005198) [B5DGE8]	3.309	0.843
CA054395	Zgc: 112247 [AAH95705; *Danio rerio*]	92 (79%)	4e-34	Pyridoxal phosphate binding; transferase activity, transferring nitrogenous groups (GO:0030170; GO:0016769) [Q502G6]	3.305	1.132
CB511966	Unnamed protein product [CAG09735; *Tetraodon nigroviridis*]	104 (72%)	7e-38	Copper ion binding; oxidoreductase activity (GO:0005507; GO:0016491) [Q4RPE7]	3.304	0.692
CB510698	Hypothetical protein [ACH85281; *Salmo salar*]	101 (70%)	4e-36	Unknown [B5RI40]	3.303	0.321
CA056659	Onmycontig mRNA sequence [EZ909005; *Oncorhynchus mykiss*] (N)	715 (97%)	0	Unknown	3.294	0.493
CB496707	Brain protein 44-like protein [ACI69379; *Salmo salar*]	72 (100%)	7e-34	Unknown [B5XEV9]	3.290	0.553
CA347004	Ribosomal RNA methyltransferase 2 [ACO08707; *Oncorhynchus mykiss*]	109 (94%)	2e-103	RNA methyltransferase activity; nucleic acid binding (GO:0008173; GO:0003676) [C1BI54]	3.287	1.012
CA386695	Novel protein similar to vertebrate	144 (97%)	2e-74	Cellular Component: integral to	3.285	0.826

	NCK-associated protein 1 [CAQ14913; *Danio rerio*]			membrane; lamellipodium membrane (GO:0016021; GO:0031258) [B0S6R1]		
EG879176	Hypothetical protein [ACH85281; *Salmo salar*]	164 (79%)	1e-60	Unknown [B5RI40]	3.284	0.858
EG789550	Chromosome 20 open reading frame 149 [ACH70875; *Salmo salar*]	121 (91%)	2e-49	Biological Process: cell differentiation; multicellular organismal development (GO:0030154; GO:0007275) [B5DGK1]	3.263	1.005
CB491414	Unnamed protein product [CAF97930; *Tetraodon nigroviridis*]	120 (82%)	3e-50	Cellular Component: cytoplasm (GO:0005737) [Q4SN52]	3.253	0.544
CB496842	C type lectin receptor B [ACM80352; *Oncorhynchus mykiss*]	92 (100%)	9e-52	Receptor activity; sugar binding (GO:0004872; GO:0005529) [C0KIP4]	3.243	0.481
CB511048	C-type lectin domain family 4 member E [ACI67923; *Salmo salar*]	27 (100%)	1e-08	Sugar binding (GO:0005529) [B5XAQ3]	3.241	0.281
CB514460	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*]	200 (100%)	2e-110	NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]	3.237	0.262
CA045270	U3 small nucleolar ribonucleoprotein protein IMP4 [ACI66547; *Salmo salar*]	205 (99%)	7e-113	Nucleic acid binding (GO:0003676) [B5X6S7]	3.228	0.337
EG927424	SJCHGC03032 protein [AAX28478; *Schistosoma japonicum*]	113 (46%)	5e-14	Unknown [Q5BVU7]	3.226	1.305
DW579188	Disulfide-isomerase A6 precursor [ACI34364; *Salmo salar*]	229 (100%)	6e-117	Isomerase activity (GO:0016853) [B5X4Y3]	3.221	0.569
DY695585	Transmembrane 9 superfamily member 2 precursor putative mRNA [BT058975; *Salmo salar*] (N)	332 (99%)	6e-164	Cellular Component: integral to membrane (GO:0016021) [C0H9G9]	3.216	0.407
CB505995	Transmembrane protein 127 putative mRNA [BT045429; *Salmo salar*] (N)	434 (100%)	0	Cellular Component: integral to membrane (GO:0016021) [B5X310]	3.210	0.969
FC072839	Unknown				3.207	1.302

CB497823	26S protease regulatory subunit 8 [ACO09830; *Osmerus mordax*]	137 (99%)	2e-70	ATP binding; nucleoside-triphosphatase activity; peptidase activity (GO:0005524; GO:0017111; GO:0008233) [C1BLC7]	3.202	0.425
CX142820	Unnamed protein product [CAG02814; *Tetraodon nigroviridis*]	221 (48%)	2e-45	Unknown [Q4S968]	3.196	0.297
CA044961	Mu-crystallin homolog [ACM08876; *Salmo salar*]	149 (100%)	1e-78	Binding; catalytic activity (GO:0005488; GO:0003824) [B9EMX9]	3.195	0.352
CX354519	Complement C1q-like protein 2 precursor [ACI66815; *Salmo salar*]	159 (100%)	1e-80	Unknown [B5X7J5]	3.185	1.235
CA062183	K18, simple type I keratin [CAA74664; *Oncorhynchus mykiss*]	105 (99%)	2e-41	Structural molecule activity (GO:0005198) [O57607]	3.182	0.119
CB516894	Onmycontig mRNA sequence [EZ780064; *Oncorhynchus mykiss*] (N)	757 (89%)	0	Unknown	3.161	0.258
CA057703	Tetraspanin-1 putative mRNA [BT060283; *Salmo salar*] (N)	493 (99%)	0	Cellular Component: integral to membrane (GO:0016021) [B9EL72]	3.155	0.604
CB508394	Oocyte protease inhibitor-2 [AAO16105; *Oncorhynchus mykiss*]	89 (76%)	2e-33	Peptidase activity (GO:0008233) [Q8AX91]	3.155	0.555
CB514430	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 [ACH85363; *Salmo salar*]	207 (83%)	2e-72	ATP binding; ATP-dependent helicase activity; RNA binding (GO:0005524; GO:0008026; GO:0003723) [B5RIC3]	3.151	0.964
CA040785	Onmycontig mRNA sequence [EZ883529; *Oncorhynchus mykiss*] (N)	664 (91%)	0	Unknown	3.145	0.618
EG825034	Membrane-spanning 4-domains subfamily A member 4A [ACI69003; *Salmo salar*]	139 (41%)	1e-14	Cellular Component: integral to membrane (GO:0016021) [B5XDT3]	3.140	0.850
CB496785	Carboxylic ester hydrolase [AAA67523; *Salmo salar*]	165 (87%)	3e-84	Carboxylesterase activity (GO:0004091) [Q92149]	3.137	0.350
CB498321	Elongation factor 2 [ACN10751; *Salmo salar*]	211 (99%)	9e-104	GTP binding; GTPase activity; translation elongation factor activity (GO:0005525; GO:0003924; GO:0003746) [C0H9N2]	3.119	1.152

CA049981	Selenoprotein Pa precursor putative mRNA [BT072221; *Salmo salar*] (N)	583 (99%)	0	Unknown	3.118	0.397
CB492757	Pentraxin [CAA67764; *Oncorhynchus mykiss*]	160 (99%)	6e-90	Unknown [P79899]	3.117	0.431
CB498020	Onmycontig mRNA sequence [EZ763824; *Oncorhynchus mykiss*] (N)	578 (98%)	0	Unknown	3.116	0.118
CA052800	THO complex 1 [AAH54938; *Danio rerio*]	201 (85%)	2e-91	Protein binding (GO:0005515) [Q7SYB2]	3.113	0.506
CB510040	Hypothetical protein mRNA [BT043964; *Salmo salar*] (N)	639 (98%)	0	Unknown [B5RI40]	3.112	0.342
CA050720	Clone ssal-rgf-001-077 [BT071827; *Salmo salar*] (N)	711 (99%)	0	Unknown	3.107	0.413
CA042760	Onmycontig mRNA sequence [EZ910931; *Oncorhynchus mykiss*] (N)	307 (89%)	3e-97	Unknown	3.099	0.565
CB497579	Glutathione S-transferase [BAA76974; *Oncorhynchus nerka*]	159 (97%)	2e-84	Glutathione transferase activity (GO:0004364) [Q9W647]	3.096	0.351
CA770758	Onmycontig mRNA sequence [EZ908703; *Oncorhynchus mykiss*] (N)	509 (90%)	2e-174	Unknown	3.087	0.512
EG770962	Ferritin, heavy subunit [ACN10128; *Salmo salar*]	175 (99%)	1e-97	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [C0H7V9]	3.073	0.433
CK991233	Onmycontig mRNA sequence [EZ907370; *Oncorhynchus mykiss*] (N)	168 (95%)	1e-64	Unknown	3.061	0.220
EG864766	Calmodulin 2 [AAX37095; *synthetic construct*]	149 (100%)	5e-79	Unknown	3.061	0.763
CB497425	Osteopontin-like protein [AAG35656|AF204760; *Oncorhynchus mykiss*]	30 (100%)	5e-08	Unknown [Q9DE42]	3.059	0.368
CB497524	Onmycontig mRNA sequence [EZ764258; *Oncorhynchus mykiss*] (N)	595 (99%)	0	Unknown	3.055	0.606
CA044880	Glutathione S-transferase theta-1 [ACI33850; *Salmo salar*]	155 (100%)	3e-83	Transferase activity (GO:0016740) [B5X3G9]	3.055	0.834
EG781251	Homeobox protien HoxB5ab [ABW77478; *Salmo salar*]	82 (100%)	4e-41	Sequence-specific DNA binding; sequence-specific DNA binding transcription factor activity (GO:0043565; GO:0003700)	3.049	0.446

				[B3TDB6]		
CK991304	Onmycontig mRNA sequence [EZ768570; *Oncorhynchus mykiss*] (N)	455 (95%)	0	Unknown	3.049	0.493
CB494082	Onmycontig mRNA sequence [EZ763960; *Oncorhynchus mykiss*] (N)	564 (97%)	0	Unknown	3.038	0.576
CK991252	Gamma-aminobutyric acid receptor-associated protein-like 2 putative mRNA [BT056984; *Salmo salar*] (N)	457 (89%)	6e-143	Receptor activity (GO:0004872) [B9EMV9]	3.026	0.465
CB498077	Ferritin, heavy subunit [ACO07472; *Oncorhynchus mykiss*]	126 (100%)	2e-86	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [C1BEL9]	3.019	0.507
CA352182	Splicing factor, arginine/serine-rich 1 putative mRNA [BT059149; *Salmo salar*] (N)	530 (95%)	0	Nucleic acid binding; nucleotide binding (GO:0003676; GO:0000166) [C0H9Z3]	3.017	0.746
DY736547	Onmycontig mRNA sequence [EZ905677; *Oncorhynchus mykiss*] (N)	579 (90%)	0	Unknown	3.013	0.744
DY721630	Onmycontig mRNA sequence [EZ888359; *Oncorhynchus mykiss*] (N)	156 (88%)	3e-41	Unknown	3.013	0.846
CA061403	Alanine aminotransferase 2-like putative mRNA [BT072409; *Salmo salar*] (N)	627 (99%)	0	Unknown	3.010	0.437
CB515030	Tumor protein p53 binding protein [AAV32965; *Oncorhynchus mykiss*]	205 (99%)	3e-118	Cellular Component: intracellular (GO:0005622) [Q5UTF0]	3.008	0.622
CA350134	Onmycontig mRNA sequence [EZ832254; *Oncorhynchus mykiss*] (N)	438 (96%)	0	Unknown	2.997	0.716
CB498357	T-complex protein 1 subunit epsilon [ACN11333; *Salmo salar*]	109 (100%)	8e-54	ATP binding; unfolded protein binding (GO:0005524; GO:0051082) [C0HBB4]	2.990	0.542
CA050681	Transposase-like mRNA [BT043992; *Salmo salar*] (N)	748 (99%)	0	DNA binding; transposase activity (GO:0003677; GO:0004803) [B5RI68]	2.981	0.455
CB494688	Novel protein [CAX14472; *Danio rerio*]	42 (79%)	7e-10	Methyltransferase activity (GO:0008168) [B8JM82]	2.980	0.454
CB497396	Pentraxin [CAA67764; *Oncorhynchus mykiss*]	141 (99%)	5e-78	Unknown [P79899]	2.975	0.488
CB497026	Cathepsin L1 precursor [ACO15730; *Caligus clemensi*]	131 (100%)	2e-73	Cysteine-type endopeptidase activity (GO:0004197)	2.971	0.471

				[C1C377]		
CB497884	Ferritin, middle subunit [ACI67714; *Salmo salar*]	138 (100%)	1e-74	Ferric iron binding (GO:0008199) [B5XA44]	2.969	0.268
CB502763	Onmycontig mRNA sequence [EZ772458; *Oncorhynchus mykiss*] (N)	592 (94%)	0	Unknown	2.957	0.923
CB493401	Nucleoside diphosphate kinase [AAO42980; *Oncorhynchus mykiss*]	151 (99%)	4e-82	ATP binding; nucleoside diphosphate kinase activity (GO:0005524; GO:0004550) [Q804Y0]	2.957	0.510
CB509527	Unnamed protein product [CAF92600; *Tetraodon nigroviridis*]	211 (61%)	2e-60	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q4T3D2]	2.949	0.450
CB503106	Y-box binding protein [ACL31579; *Oncorhynchus mykiss*]	71 (100%)	1e-21	DNA binding (GO:0003677) [B8Y7S9]	2.944	0.542
CB493361	Toxin-1 [AAM21198|AF363273; *Oncorhynchus mykiss*]	61 (87%)	1e-26	Unknown [Q8JJ66]	2.942	0.712
CB503706	Cold-inducible RNA-binding protein putative mRNA [BT125559; *Salmo salar*] (N)	593 (99%)	0	Unknown	2.938	0.378
CB509786	Novel protein [CAI21251; *Danio rerio*]	170 (46%)	7e-36	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q5RIH8]	2.937	0.838
CA038043	Onmycontig mRNA sequence [EZ764913; *Oncorhynchus mykiss*] (N)	509 (95%)	0	Unknown	2.934	0.320
CA054781	Onmycontig mRNA sequence [EZ781014; *Oncorhynchus mykiss*] (N)	514 (92%)	0	Unknown	2.921	0.686
CB497992	Ovomucin alpha-subunit [BAB2148; *Gallus gallus*]	141 (42%)	1e-28	Unknown	2.916	0.394
EG776495	SJCHGC03032 protein [AAX28478; *Schistosoma japonicum*]	101 (49%)	2e-14	Unknown [Q5BVU7]	2.906	0.611
CB501000	Apolipoprotein C-I precursor [ACI69086; *Salmo salar*]	87 (99%)	9e-41	Cellular Component: extracellular region (GO:0005576) [B5XE16]	2.887	0.351
CA040448	Extracellular matrix protein 1 precursor putative mRNA [BT059193; *Salmo salar*] (N)	568 (99%)	0	Cellular Component: extracellular space (GO:0005615) [C0HA37]	2.885	0.642
CA059110	Onmycontig mRNA sequence	453 (96%)	0	Unknown	2.883	0.407

	[EZ783117; *Oncorhynchus mykiss*] (N)					
CB491425	CTP synthase 1 [ACI34065; *Salmo salar*]	133 (97%)	4e-79	CTP synthase activity (GO:0003883) [B5X434]	2.877	0.194
CA040196	Integral membrane protein 2B putative mRNA [BT058945; *Salmo salar*] (N)	623 (99%)	0	Unknown [C0H9D9]	2.872	0.194
CA061826	Transposase-like mRNA [BT043992; *Salmo salar*] (N)	714 (100%)	0	DNA binding; transposase activity (GO:0003677; GO:0004803) [B5RI68]	2.866	0.296
CA050891	TCR-alpha/delta locus [EF467299; *Salmo salar*] (N)	292 (87%)	4e-81	Unknown	2.863	0.582
CB492604	Glutathione S-transferase A [ACO07597; *Oncorhynchus mykiss*]	48 (98%)	3e-19	Transferase activity (GO:0016740) [C1BEZ4]	2.843	0.443
CB497009	HSC71 [AAB21658; *Oncorhynchus mykiss*]	133 (100%)	3e-48	ATP binding (GO:0005524) [P08108]	2.842	0.588
DW573529	Onmycontig mRNA sequence [EZ904381; *Oncorhynchus mykiss*] (N)	390 (82%)	4e-71	Unknown	2.826	0.840
CA054597	Unknown				2.818	0.678
CX245969	Tdo2 protein [AAI51921; *Danio rerio*]	238 (83%)	2e-103	Iron ion binding; tryptophan 2,3-dioxygenase activity (GO:0005506; GO:0004833) [A7MBU6]	2.816	0.347
CK991235	Ferritin, heavy subunit [ACO07472; *Oncorhynchus mykiss*]	95 (93%)	2e-44	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [C1BEL9]	2.815	0.469
CA051262	Stress-induced-phosphoprotein 1 putative mRNA [BT044711; Salmo salar] (N)	803 (99%)	0	Binding (GO:0005488) [B5X0Z2]	2.806	0.407
CB507396	Ferritin, middle subunit [ACI68639; *Salmo salar*]	126 (100%)	5e-70	Ferric iron binding (GO:0008199) [B5XCR9]	2.804	0.283
CA387966	Liver-expressed antimicrobial peptide 2B [AAR11767; *Oncorhynchus mykiss*]	90 (99%)	7e-47	Biological Process: defense response to bacterium (GO:0042742) [Q64JE5]	2.798	0.304
CB494647	C-C motif chemokine 20 precursor [ACI66945; *Salmo salar*]	76 (91%)	2e-33	Chemokine activity (GO:0008009)[B5X7X5]	2.792	0.555
CA043387	Onmycontig mRNA sequence	596 (94%)	0	Unknown	2.788	0.047

	[EZ763364; *Oncorhynchus mykiss*] (N)					
CB497635	40S ribosomal protein S4 [ACN10029; *Salmo salar*]	177 (99%)	9e-96	Structural constituent of ribosome (GO:0003735) [C0H7L0]	2.775	0.485
CB491826	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*]	162 (99%)	2e-85	NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]	2.773	0.465
CB494461	Onmycontig mRNA sequence [EZ763389; *Oncorhynchus mykiss*] (N)	596 (99%)	0	Unknown	2.768	0.638
CB497061	Onmycontig mRNA sequence [EZ799738; *Oncorhynchus mykiss*] (N)	602 (99%)	0	Unknown	2.765	0.388
CB514705	Fructose-bisphosphate aldolase A [ACN10700; *Salmo salar*]	136 (100%)	3e-74	Fructose-bisphosphate aldolase activity (GO:0004332) [C0H9I1]	2.762	0.653
CK991077	DNA-directed RNA polymerases I, II, and III subunit RPABC2 putative mRNA [BT057259; *Salmo salar*] (N)	617 (99%)	0	DNA binding; DNA-directed RNA polymerase activity (GO:0003677; GO:0003899) [B9ENN4]	2.748	0.310
CK991242	Adult-type muscle actin 2 [CAX48983; *Botryllus schlosseri*]	52 (91%)	8e-20	ATP binding; protein binding (GO:0005524; GO:0005515) [C0MP46]	2.745	0.528
CB515170	Zgc: 101080 [AAH78275; *Danio rerio*]	68 (68%)	5e-11	Cellular Component: centrosome; gamma-tubulin ring complex; spindle (GO:0005813; GO:0008274; GO:0005819) [Q6DC17]	2.741	0.439
CA038031	Beta-2-glycoprotein 1 precursor [ACN10110; *Salmo salar*]	132 (96%)	1e-71	Unknown [C0H7U1]	2.739	0.266
CK990883	Embryonic beta-type globin2 [BAA34951; *Oncorhynchus mykiss*]	131 (89%)	2e-59	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [Q9YGF4]	2.736	0.328
CB506201	Ferritin, middle subunit [ACI33572; *Salmo salar*]	106 (100%)	3e-56	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491)	2.725	0.716

				[B5X2P1]		
CA050886	Glyceraldehyde-3-phosphate dehydrogenase [ACI69846; *Salmo salar*]	157 (100%)	6e-85	NAD or NADH binding; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity (GO:0051287; GO:0004365) [B5XG76]	2.714	0.258
CA060499	60S ribosomal protein L10a [ACI69173; *Salmo salar*]	159 (99%)	3e-72	RNA binding (GO:0003723) [B5XEA3]	2.713	0.233
EG819054	Onmycontig mRNA sequence [EZ783551; *Oncorhynchus mykiss*] (N)	341 (83%)	4e-71	Unknown	2.700	0.521
CK991221	Onmycontig mRNA sequence [EZ764029; *Oncorhynchus mykiss*] (N)	383 (96%)	5e-174	Unknown	2.698	0.580
EG863793	Integral membrane protein 2B [ACN10658; *Salmo salar*]	108 (99%)	8e-56	Unknown [C0H9D9]	2.691	0.401
DY732989	Zgc: 85729 [AAH70008; *Danio rerio*]	208 (99%)	3e-120	Phosphoprotein phosphatase activity (GO:0004721) [Q6NSN6;]	2.689	0.599
CB510571	Apolipoprotein A-I-1 precursor [ACI69572; *Salmo salar*]	148 (100%)	3e-58	Lipid binding (GO:0008289) [B5XFF2]	2.686	0.767
DY696542	Ferritin, middle subunit putative mRNA [BT059824; *Salmo salar*] (N)	302 (92%)	5e-110	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [C0H718]	2.685	0.381
CB497602	Heat shock protein 70 isoform 3 [ACH70704; *Salmo salar*]	108 (99%)	1e-54	ATP binding (GO:0005524) [B5DG30]	2.683	0.332
CA041338	Beta-2 microglobulin type 2 [AAP51056; *Oncorhynchus mykiss*]	64 (97%)	4e-37	Cellular Component: MHC class I protein complex (GO:0042612) [Q6XQ10]	2.679	0.309
CA038770	C-type MBL-2 protein [CAJ14130; *Oncorhynchus mykiss*]	43 (96%)	9e-19	Sugar binding (GO:0005529) [Q4LAN6]	2.666	0.439
CB497343	Unnamed protein product [CAF99287; *Tetraodon nigroviridis*]	39 (95%)	4e-14	Protein binding; zinc ion binding (GO:0005515; GO:0008270) [Q4SJ95]	2.657	0.310
CK991275	Brain protein 44-like protein [ACO07659; *Oncorhynchus mykiss*]	71 (96%)	5e-31	Unknown [C1BF56]	2.650	0.115

CK990626	Beta-2-microglobulin precursor putative mRNA [BT046451; *Salmo salar*] (N)	552 (99%)	0	Unknown [B5X5Y2]	2.650	0.409
CB514575	Transport protein Sec61 subunit alpha isoform B putative mRNA [BT072062; *Salmo salar*] (N)	759 (99%)	0	Unknown	2.627	0.305
CA061219	Onmycontig mRNA sequence [EZ771593; *Oncorhynchus mykiss*] (N)	732 (91%)	0	Unknown	2.619	0.516
CB496845	Small EDRK-rich factor 2 [ACO07539; *Oncorhynchus mykiss*]	61 (100%)	2e-26	Unknown [C1BET6]	2.617	0.312
CB516814	Hypothetical membrane associated protein [ABE00674; *Lactobacillus salivarius* UCC118]	29 (69%)	3e-06	Unknown [Q1WR24]	2.616	0.372
CX257451	Ldhb protein [AAH44190; *Danio rerio*]	97 (84%)	3e-41	L-lactate dehydrogenase activity; binding (GO:0004459; GO:0005488) [Q803U5]	2.614	0.252
CA059252	Onmycontig mRNA sequence [EZ765737; *Oncorhynchus mykiss*] (N)	689 (95%)	0	Unknown	2.608	0.459
CB497385	Onmycontig mRNA sequence [EZ763364; *Oncorhynchus mykiss*] (N)	558 (99%)	0	Unknown	2.607	0.355
CB492978	40S ribosomal protein S27 [ABJ98653; *Psetta maxima*]	87 (98%)	2e-37	Metal ion binding; structural constituent of ribosome (GO:0046872; GO:0003735) [A0EZY9]	2.605	0.573
CB496934	Onmycontig mRNA sequence [EZ907372; *Oncorhynchus mykiss*] (N)	616 (99%)	0	Unknown	2.602	0.087
CA042790	60S ribosomal protein L3 [ACI68315; *Salmo salar*]	123 (99%)	5e-68	Structural constituent of ribosome (GO:0003735) [B5XBU5]	2.596	0.268
CB509453	Ribosomal protein L3-like [ACH70797; *Salmo salar*]	169 (100%)	4e-96	Structural constituent of ribosome (GO:0003735) [B5DGC3]	2.588	0.316
DW566777	Interferon alpha 1-like gene, complete sequence; growth hormone 1 gene, complete cds; and skeletal muscle sodium channel alpha subunit-like, myosin alkali light chain-like, and microtubule-associated protein Tau-like genes, complete sequence	347 (90%)	1e-114	Hormone activity (GO:0005179) [Q5SDS1]	2.584	0.224

	[EU621898; *Salmo salar*] [(N)]					
CB497380	Onmycontig mRNA sequence [EZ905653; *Oncorhynchus mykiss*] [(N)]	620 (99%)	0	Unknown	2.583	0.293
EG927569	Onmycontig mRNA sequence [EZ885295; *Oncorhynchus mykiss*] [(N)]	305 (87%)	2e-86	Unknown	2.582	0.508
CB496385	Onmycontig mRNA sequence [EZ763477; *Oncorhynchus mykiss*] [(N)]	617 (99%)	0	Unknown	2.579	0.554
CB496604	Hemoglobin subunit beta [ACO07479; *Oncorhynchus mykiss*]	148 (100%)	6e-80	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BEM6]	2.572	0.428
CB502520	Calmodulin putative mRNA [BT125331; Salmo salar] [(N)]	798 (99%)	0	Unknown	2.570	0.347
CA054146	Onmycontig mRNA sequence [EZ795941; *Oncorhynchus mykiss*] [(N)]	727 (90%)	0	Unknown	2.567	0.740
CA044775	Onmycontig mRNA sequence [EZ871736; *Oncorhynchus mykiss*] [(N)]	292 (91%)	5e-98	Unknown	2.556	0.241
CB516765	Fish-egg lectin [ACN10420; *Salmo salar*]	118 (100%)	4e-60	Sugar binding (GO:0005529) [C0H8Q1]	2.554	0.212
CB497693	Thymosin beta-12 [ACI67890; *Salmo salar*]	43 (98%)	2e-07	Actin binding (GO:0003779) [B5X6X6]	2.540	0.529
DY732776	Histone H3.3 putative mRNA [BT125234; *Salmo salar*] [(N)]	385 (95%)	2e-162	Unknown	2.540	0.523
CK991031	Ferritin, middle subunit [ACI68839; *Salmo salar*]	90 (88%)	6e-37	Ferric iron binding (GO:0008199) [B5XDB9]	2.539	0.390
CB494566	Nascent polypeptide-associated complex subunit alpha [ACI69238; *Salmo salar*]	109 (100%)	1e-37	Unknown [B5XEG8]	2.538	0.451
CB496642	Microsomal glutathione S-transferase 3 [ACO08637; *Oncorhynchus mykiss*]	122 (100%)	2e-67	Transferase activity (GO:0016740) [C1BHY4]	2.530	0.416
EG898351	Onmycontig mRNA sequence [EZ763364; *Oncorhynchus mykiss*] [(N)]	757 (94%)	0	Unknown	2.522	0.372
EG910777	Unnamed protein product [CAG05847; *Tetraodon nigroviridis*]	36 (70%)	3e-06	GTP binding (GO:0005525) [Q4S0I5]	2.518	0.174
EG914919	Unnamed protein product [BAG59611; *Homo sapiens*]	141 (27%)	8e-07	Cellular Component: integral to membrane (GO:0016021) [B4DLP9]	2.515	0.324

CA062582	Zinc transporter 7 putative mRNA [BT045478; *Salmo salar*] (N)	653 (99%)	0	Cation transmembrane transporter activity (GO:0008324) [B5X359]	2.511	0.434
CA059976	Brain protein 44-like protein [ACI66404; *Salmo salar*]	103 (100%)	4e-54	Unknown [B5X6D4]	2.508	0.425
CB493962	Fructose-bisphosphate aldolase B [ACN10100; *Salmo salar*]	48 (90%)	2e-15	Fructose-bisphosphate aldolase activity (GO:0004332) [C0H7T1]	2.503	0.278
CK990679	Onmycontig mRNA sequence [EZ764857; *Oncorhynchus mykiss*] (N)	470 (93%)	0	Unknown	2.501	0.445
CB505797	RCC2 homolog [ACI33792; *Salmo salar*]	56 (75%)	3e-26	DNA binding; transposase activity (GO:0003677; GO:0004803) [B5X3B1]	2.498	0.333
CB493265	Adenine nucleotide translocator s598 [BAD86711; *Takifugu rubripes*]	41 (88%)	2e-23	Binding; transporter activity (GO:0005488 GO:0005215) [Q5KSP2]	2.492	0.251
CA058509	Ancient ubiquitous protein 1 precursor [ACI33926; *Salmo salar*]	38 (93%)	4e-12	Acyltransferase activity (GO:0008415) [B5X3P5]	2.485	0.499
CB494527	Sporozoite surface protein 2 precursor [ACI33544; *Salmo salar*]	82 (49%)	6e-06	Unknown [B5X2L3]	2.484	0.539
EG780477	Unknown				2.467	0.397
EG898703	Beta actin isoform 1 [BAG12566; *Solea senegalensis*]	244 (96%)	2e-130	ATP binding; protein binding (GO:0005524; GO:0005515) [B1B560]	2.465	0.127
FC072797	Hemoglobin subunit beta [ACI68762; *Salmo salar*]	94 (91%)	9e-38	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [B5XD42]	2.456	0.410
CA056744	Ferritin, middle subunit [ACI66713; *Salmo salar*]	181 (99%)	8e-100	Ferric iron binding (GO:0008199) [B5X793]	2.449	0.106
CK991318	ATP synthase H+ transporting mitochondrial F1 complex beta [ACH85277; *Salmo salar*]	56 (88%)	4e-19	ATP binding; hydrogen ion transporting ATP synthase activity, rotational mechanism; hydrogen-exporting ATPase activity, phosphorylative mechanism; proton-transporting ATPase activity, rotational	2.448	0.327

				mechanism (GO:0005524; GO:0046933; GO:0008553; GO:0046961) [B5RI36]		
EG790867	Unknown				2.446	0.195
CA044962	Onmycontig mRNA sequence [EZ763684; *Oncorhynchus mykiss*] (N)	571 (97%)	0	Unknown	2.438	0.198
CA059829	Eukaryotic translation initiation factor 3 subunit 3 [ACO08262; *Oncorhynchus mykiss*]	106 (99%)	5e-45	Translation initiation factor activity (GO:0003743) [C1BGV9]	2.436	0.317
EG813231	Heat shock protein 70 isoform 3 [ACH70704; *Salmo salar*]	111 (100%)	2e-56	ATP binding (GO:0005524) [B5DG30]	2.435	0.384
CB512930	Transport protein Sec61 subunit beta [ACI69157; *Salmo salar*]	98 (100%)	1e-25	Unknown [B5XE87]	2.434	0.199
CA042642	Malate dehydrogenase, mitochondrial precursor [ACI66104; *Salmo salar*]	130 (100%)	4e-66	L-malate dehydrogenase activity (GO:0030060) [B5X5I4]	2.426	0.273
CB486281	Ferritin heavy subunit [AAB34575; *Salmo salar*]	120 (94%)	1e-65	Ferric iron binding; ferroxidase activity (GO:0008199; GO:0004322) [P49946]	2.424	0.352
CB502636	Membrane-spanning 4-domains subfamily A member 4A [ACI69003; *Salmo salar*]	67 (98%)	4e-30	Cellular Component: integral to membrane (GO:0016021) [B5XDT3]	2.419	0.465
EG858633	Onmycontig mRNA sequence [EZ801426; *Oncorhynchus mykiss*] (N)	744 (93%)	0	Unknown	2.417	0.682
DY703721	Onmycontig mRNA sequence [EZ905927; *Oncorhynchus mykiss*] (N)	675 (92%)	0	Unknown	2.413	0.449
CA054940	Glutathione S-transferase P [ACI70112; *Salmo salar*]	62 (100%)	4e-28	Glutathione transferase activity (GO:0004364) [B5XGZ2]	2.412	0.229
CB509536	Onmycontig mRNA sequence [EZ774133; *Oncorhynchus mykiss*] (N)	179 (98%)	4e-79	Unknown	2.409	0.193
CA037526	Chibby homolog 1 [ACI68079; *Salmo salar*]	117 (100%)	2e-41	Unknown [B5XB59]	2.402	0.353
CB501401	Beta-2-microglobulin precursor [ACM08831; *Salmo salar*]	49 (100%)	2e-20	Cellular Component: MHC class I protein complex (GO:0042612) [B9EMT4]	2.398	0.361
CK991113	Type I keratin S8 [CAC45059; *Oncorhynchus mykiss*]	88 (97%)	1e-39	Structural molecule activity (GO:0005198) [Q90W73]	2.398	0.441
CA037616	Complement factor H1 protein	154 (79%)	4e-68	Unknown [Q4QZ18]	2.389	0.519

	[CAJ01769; *Oncorhynchus mykiss*]					
CB509551	Thymosin beta-12 [ACI67890; *Salmo salar*]	43 (100%)	2e-08	Actin binding (GO:0003779) [B5X6X6]	2.386	0.224
DY732771	26S proteasome non-ATPase regulatory subunit 3 putative mRNA [BT059067; *Salmo salar*] (N)	127 (100%)	1e-58	Enzyme regulator activity (GO:0030234) [C0H9R1]	2.373	0.329
CB502821	Physical map contig 483 [EU481821; *Salmo salar*] (N)	135 (90%)	2e-38	Unknown	2.365	0.450
CB496844	Wu: fc47e12 protein [AAI07829; *Danio rerio*]	59 (90%)	4e-25	Oxidoreductase activity, acting on the CH-CH group of donors (GO:0016627) [Q3B743]	2.365	0.188
CA041519	Glutathione S-transferase theta-1 [ACI66470; *Salmo salar*]	157 (100%)	3e-84	Transferase activity (GO:0016740) [B5X6K0]	2.354	0.238
CB517969	Transposable element Tcb2 transposase [ACI67316; *Salmo salar*]	74 (84%)	2e-33	Unknown [B5X8Z6]	2.349	0.481
CA044682	Onmycontig mRNA sequence [EZ763364; *Oncorhynchus mykiss*] (N)	275 (95%)	3e-115	Unknown	2.348	0.410
EG822917	GTP cyclohydrolase 1 feedback regulatory protein [ACI69203; *Salmo salar*]	89 (100%)	4e-45	Hydrolase activity; protein binding (GO:0016787; GO:0005515) [B5XED3]	2.348	0.225
CA052820	Onmycontig mRNA sequence [EZ870780; *Oncorhynchus mykiss*] (N)	520 (87%)	6e-153	Unknown	2.347	0.248
CB509736	Eukaryotic translation initiation factor 3, subunit H mRNA [BT043978; *Salmo salar*] (N)	290 (99%)	2e-147	Translation initiation factor activity (GO:0003743) [B5RI54]	2.345	0.252
CN442541	Ferritin, middle subunit [ACO07744; *Oncorhynchus mykiss*]	124 (100%)	5e-66	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [C1BFE1]	2.332	0.195
CK990766	Adenosylhomocysteinase B putative mRNA [BT058783; *Salmo salar*] (N)	659 (95%)	0	Adenosylhomocysteinase activity; binding (GO:0004013; GO:0005488) [B5DGE0]	2.330	0.368
CA356917	Novel protein (zgc: 153086) [CAQ13556; *Danio rerio*]	159 (68%)	3e-51	Unknown [B0S713]	2.326	0.268
CK990457	Hemoglobin subunit beta-1 [ACN09863; *Salmo salar*]	98 (100%)	4e-48	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825;	2.322	0.448

				GO:0005344) [C0H744]		
CA041873	Alpha-6-fucosyltransferase [CAH03675; *Danio rerio*]	46 (70%)	7e-11	Glycoprotein 6-alpha-L-fucosyltransferase activity (GO:0008424) [Q6EV75]	2.319	0.307
CB496899	Histone H1.0 [ACN10192; *Salmo salar*]	101 (98%)	2e-50	DNA binding (GO:0003677) [C0H823]	2.307	0.313
CA057803	Cell-surface antigen heavy chain putative mRNA [BT059429; *Salmo salar*] (N)	584 (99%)	0	Catalytic activity; cation binding (GO:0003824; GO:0043169) [C0HAS3]	2.285	0.187
CA038180	NADH dehydrogenase 1 alpha subcomplex subunit 2 [ACI68755; *Salmo salar*]	94 (100%)	9e-47	Cellular Component: mitochondrial inner membrane; respiratory chain (GO:0005743; GO:0070469) [B5XD35]	2.282	0.222
CB496981	DNA-directed RNA polymerases I, II, and III subunit RPABC2 [ACO13758; *Esox lucius*]	56 (99%)	2e-24	DNA binding; DNA-directed RNA polymerase activity (GO:0003677; GO:0003899) [C1BXK5]	2.282	0.398
CA058630	Catalase putative mRNA [BT045615; *Salmo salar*] (N)	763 (99%)	0	Catalase activity; heme binding (GO:0004096; GO:0020037) [B5X3J6]	2.281	0.174
CB503707	Heat shock protein hsp90 beta [AAD30275|AF135117; *Salmo salar*]	85 (100%)	3e-41	ATP binding; unfolded protein binding (GO:0005524; GO:0051082) [Q9W6K6]	2.280	0.119
CB514814	Nucleoside phosphorylase [AAH66610; *Danio rerio*]	77 (84%)	1e-29	Purine-nucleoside phosphorylase activity (GO:0004731) [Q6NYG0]	2.272	0.456
CA057311	Delta-5 fatty acyl desaturase (D5fad) gene [GU294485; *Salmo salar*] (N)	606 (100%)	0	Oxidoreductase activity (GO:0016491) [D2Y360]	2.254	0.241
CB497163	Guanine nucleotide binding protein beta polypeptide 2-like 1 [ACH70647; *Salmo salar*]	174 (99%)	5e-113	Unknown [B5DFX3]	2.253	0.210
CB499573	Unnamed protein product [CAG06430; *Tetraodon nigroviridis*]	139 (66%)	6e-33	Unknown [Q4RYV2]	2.251	0.371
CB493489	Onmycontig mRNA sequence [EZ826281; *Oncorhynchus nerka*] (N)	655 (99%)	0	Unknown	2.249	0.285
CB497481	Onmycontig mRNA sequence [EZ906965; *Oncorhynchus mykiss*] (N)	532 (99%)	0	Unknown	2.243	0.132

CB497940	UDP glucuronosyltransferase 1 family polypeptide a3 isoform 1 [ADC91921; *Danio rerio*]	231 (74%)	6e-101	Transferase activity, transferring hexosyl groups (GO:0016758) [D3XD50]	2.234	0.072
CB509675	Actin [AAK60616|AF330142; *Oncorhynchus mykiss*]	110 (100%)	3e-57	ATP binding; protein binding (GO:0005524; GO:0005515) [Q90WC5]	2.231	0.386
CA045289	Unknown				2.229	0.259
CK990503	Unknown				2.227	0.468
DY715202	Elongation factor 2 [ACN58670; *Salmo salar*]	65 (77%)	4e-20	GTP binding; translation elongation factor activity (GO:0005525; GO:0003746) [C0PUE5]	2.216	0.356
CA043312	Membrane-spanning 4-domains subfamily A member 8A [ACI70074; *Salmo salar*]	82 (100%)	9e-28	Cellular Component: integral to membrane (GO:0016021) [B5XGV4]	2.212	0.300
EG939661	Onmycontig mRNA sequence [EZ826103; *Oncorhynchus nerka*] (N)	240 (85%)	3e-56	Unknown	2.199	0.225
CB505628	Apolipoprotein A-I precursor [ACI68193; *Salmo salar*]	126 (100%)	3e-52	Lipid binding (GO:0008289) [B5XBH3]	2.189	0.303
CB498181	Kelch repeat and BTB (POZ) domain containing 10 [ACH70794; *Salmo salar*]	76 (97%)	8e-35	Protein binding (GO:0005515) [B5DGC0]	2.185	0.319
DW574506	Onmycontig mRNA sequence [EZ764499; *Oncorhynchus mykiss*] (N)	321 (86%)	2e-83	Unknown	2.184	0.279
EG782703	Chromosome 20 open reading frame 149 mRNA [BT043760; *Salmo salar*] (N)	725 (98%)	0	Biological Process: cell differentiation; multicellular organismal development (GO:0030154; GO:0007275) [B5DGK1]	2.174	0.219
CB491273	Onmycontig mRNA sequence [EZ764029; *Oncorhynchus mykiss*] (N)	398 (100%)	0	Unknown	2.174	0.350
EG824088	FGF2 [ACJ02099; *Salmo salar*]	27 (78%)	9e-06	Growth factor activity (GO:0008083) [C6EWZ5]	2.173	0.115
CA050489	Transposase-like mRNA [BT043992; *Salmo salar*](N)	687 (100%)	0	DNA binding; transposase activity (GO:0003677; GO:0004803) [B5RI68]	2.167	0.105
CA048859	BAC CHORI214-92I04 [EF427384;	566 (99%)	0	Threonine-type endopeptidase	2.166	0.288

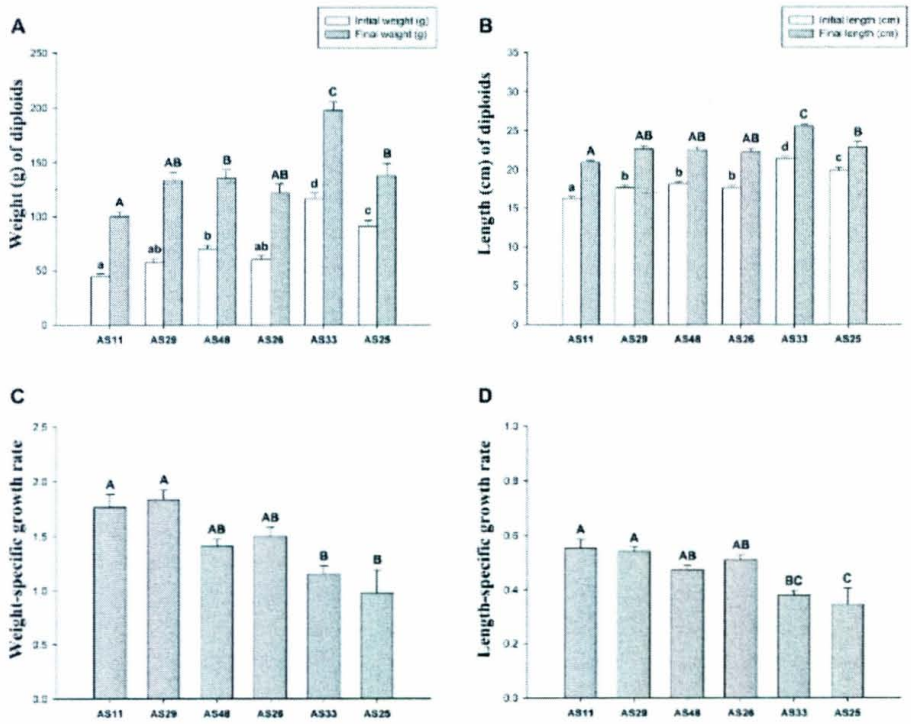
	Salmo salar] (N)			activity (GO:0004298) [A7KE01]		
CA045317	3-ketoacyl-CoA thiolase, mitochondrial putative mRNA [BT045547; *Salmo salar*] (N)	686 (99%)	0	Acyltransferase activity (GO:0008415) [B5X3C8]	2.161	0.236
CA045102	Disulfide-isomerase A3 precursor [ACI33158; *Salmo salar*]	55 (70%)	1e-10	Isomerase activity (GO:0016853) [B5X1H7]	2.150	0.223
CB492360	Onmycontig mRNA sequence [EZ764029; *Oncorhynchus mykiss*] (N)	394 (100%)	0	Unknown	2.149	0.216
DY725548	Onmycontig mRNA sequence [EZ826561; *Oncorhynchus nerka*] (N)	115 (85%)	2e-19	Unknown	2.148	0.393
CB497597	Very long-chain acyl-CoA synthetase [ACI34091; *Salmo salar*]	120 (98%)	1e-90	Catalytic activity (GO:0003824) [B5X460]	2.137	0.424
CB515855	Cytochrome b-c1 complex subunit 2, mitochondrial precursor [ACN10092; *Salmo salar*]	222 (100%)	8e-117	Metalloendopeptidase activity; zinc ion binding (GO:0004222; GO:000827) [C0H7S3]	2.134	0.241
CB496960	Unnamed protein product [CAF90593; *Tetraodon nigroviridis*]	122 (73%)	3e-44	Nucleic acid binding (GO:0003676) [Q4T939]	2.133	0.186
CB497723	Hemoglobin subunit beta-4 [ACO08020; *Oncorhynchus mykiss*]	148 (99%)	9e-79	Heme binding; oxygen binding; oxygen transporter activity (GO:0020037; GO:0019825; GO:0005344) [C1BG67]	2.126	0.357
CB501290	Transposase [ABV31711; *Salmo salar*]	59 (77%)	1e-19	DNA binding; transposase activity (GO:0003677; GO:0004803) [A8C5I4]	2.122	0.327
CA058414	Transposable element Tcb2 transposase [ACI67316; *Salmo salar*]	93 (78%)	1e-33	Unknown [B5X8Z6]	2.118	0.155
CB498335	Properdin P factor 2 [CAP17612; *Oncorhynchus mykiss*]	141 (100%)	6e-87	Unknown [A8YQG4]	2.118	0.146
CB497789	Ependymin precursor [ACI68886; *Salmo salar*]	36 (98%)	2e-12	Calcium ion binding (GO:0005509) [B5XDG6]	2.114	0.262
CA038363	Onmycontig mRNA sequence [EZ826574; *Oncorhynchus nerka*] (N)	623 (94%)	0	Unknown	2.108	0.146
EG776269	Unnamed protein product [CAF89670; *Tetraodon nigroviridis*]	136 (45%)	6e-25	Carbohydrate binding; catalytic activity (GO:0030246; GO:0003824) [Q4TBR2]	2.103	0.332

CB498370	Ferritin, middle subunit [ACO08179; *Oncorhynchus mykiss*]	113 (100%)	1e-59	Ferric iron binding; oxidoreductase activity (GO:0008199; GO:0016491) [C1BGM6]	2.094	0.072
CB492183	Onmycontig mRNA sequence [EZ826574; *Oncorhynchus mykiss*] (N)	578 (99%)	0	Unknown	2.090	0.315
CA038790	Antithrombin [CAB64714; *Salmo salar*]	145 (98%)	5e-106	Serine-type endopeptidase inhibitor activity (GO:0004867) [Q9PTA8]	2.090	0.163
CK990897	Fatty acid-binding protein, intestinal putative mRNA [BT048647; *Salmo salar*] (N)	507 (96%)	0	Lipid binding; transporter activity (GO:0008289; GO:0005215) [B5XC78]	2.086	0.185
CA061344	Onmycontig mRNA sequence [EZ871918; *Oncorhynchus mykiss*] (N)	95 (92%)	1e-25	Unknown	2.084	0.206
EG907280	IgH locus A genomic sequence [GU129139; *Salmo salar*] (N)	626 (81%)	3e-121	Unknown [D3WHV5]	2.078	0.334
CB502663	Ferritin, middle subunit [ACI69419; *Salmo salar*]	145 (99%)	2e-78	Ferric iron binding (GO:0008199) [B5XEZ9]	2.067	0.196
CB510682	Histone H1x putative mRNA [BT057601; *Salmo salar*] (N)	686 (100%)	0	DNA binding (GO:0003677) [B9EPK8]	2.067	0.132
CB502095	Unknown				2.064	0.235
CB502173	Interferon-inducible GTPase_b and interferon-inducible GTPase_a genes [EU221179; *Salmo salar*] (N)	502 (97%)	0	GTP binding; hydrolase activity, acting on acid anhydrides (GO:0005525; GO:0016817) [A8WCJ8]	2.054	0.248
CA045274	Unnamed protein product [CAG08559; *Tetraodon nigroviridis*]	114 (89%)	7e-56	Unknown [Q4RSS3]	2.053	0.155
CA051016	60S ribosomal protein L8 [ACN10341; *Salmo salar*]	220 (99%)	3e-118	Structural constituent of ribosome (GO:0003735) [C0H8H2]	2.019	0.359
CA055684	Onmycontig mRNA sequence [EZ796074; *Oncorhynchus mykiss*] (N)	479 (92%)	1e-174	Unknown	2.002	0.133
CA061778	Cytochrome P450 [ACH70691; *Salmo salar*]	97 (95%)	4e-48	Electron carrier activity; heme binding; monooxygenase activity (GO:0009055; GO:0020037; GO:0004497) [B5DG17]	1.993	0.266
CA061987	Unknown				1.974	0.286

CK990756	Fatty acid-binding protein, brain [ACO14084; *Esox lucius*]	77 (88%)	6e-30	Lipid binding; transporter activity (GO:0008289; GO:0005215) [C1BYI1]	1.973	0.229
CA060424	60S acidic ribosomal protein P0 [ACI68961; *Salmo salar*]	219 (100%)	5e-93	Structural constituent of ribosome (GO:0003735) [B5XDP1]	1.968	0.325
DY729936	Myelin protein zero-like protein 2 precursor [ACI67989; *Salmo salar*]	18 (95%)	3e-08	Cellular Component: membrane (GO:0016020) [B5XAW9]	1.899	0.201
CB492413	Apolipoprotein A-I-1 [AAB96972; *Oncorhynchus mykiss*]	103 (100%)	1e-38	Lipid binding (GO:0008289) [O57523]	1.846	0.276

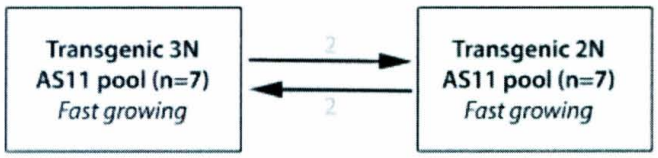
See Appendix II for footnotes.

APPENDIX XIII. Supplemental figure showing growth performance data of six diploid GH transgenic (2NGHTg) Atlantic salmon families (AS11, AS29, AS48, AS26, AS 33 and AS25) during a period of approximately 45 days. A. Initial and final weight; B. Initial and final length; C Weight-specific growth rate (SGR_W); D. Length-specific growth rate (SGR_L). All data are presented as means (± SE). For all growth parameters presented in panel A-D, different letters were used to identify significant differences (cut off $p = 0.05$) among the six families enrolled in this study. In panel A and B, significant differences in both initial weight and length among families were identified by different lower case letters and significant differences among the six families were identified by different upper case letters. In panel C and D, significant differences in weight- and length-specific growth rates among families were identified by different upper case letters.

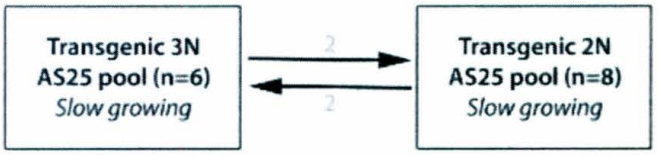

A
Initial weight (g)
Final weight (g)
Weight (g) of diploids
250
200
150
100
50
0
a
A
ab
AB
b
B
ab
AB
d
C
c
B
AS11
AS29
AS48
AS26
AS33
AS25
B
Initial length (cm)
Final length (cm)
Length (cm) of diploids
35
30
25
20
15
10
5
0
a
A
b
AB
b
AB
b
AB
d
C
c
B
C
Weight-specific growth rate
2.5
2.0
1.5
1.0
0.5
0.0
A
A
AB
AB
B
B
D
Length-specific growth rate
1.0
0.8
0.6
0.4
0.2
0.0
A
A
AB
AB
BC
C

APPENDIX XIV. Supplemental figure showing experimental design and results summary of a 32K cDNA microarray study to identify differentially expressed hepatic transcripts between diploids (2N) and triploids (3N) in three GHTg families. Within each comparison, microarray features with more than 2-fold higher expression in a given comparison (e.g. AS11 2N vs. 3N) in any three (including one dye-swap) out of four technical replicate arrays (two duplicates, two dye-swaps). The base of each arrow represents Cy3-labeled target and the head of each arrow represents the Cy5-labeled target.

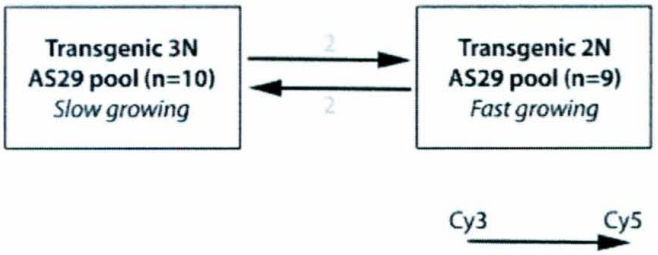
AS11: 2N > 3N (any 3 out of 4 slides): 46 microarray features (Appendix VII)
3N > 2N (any 3 out of 4 slides): 133 microarray features (Appendix VIII)



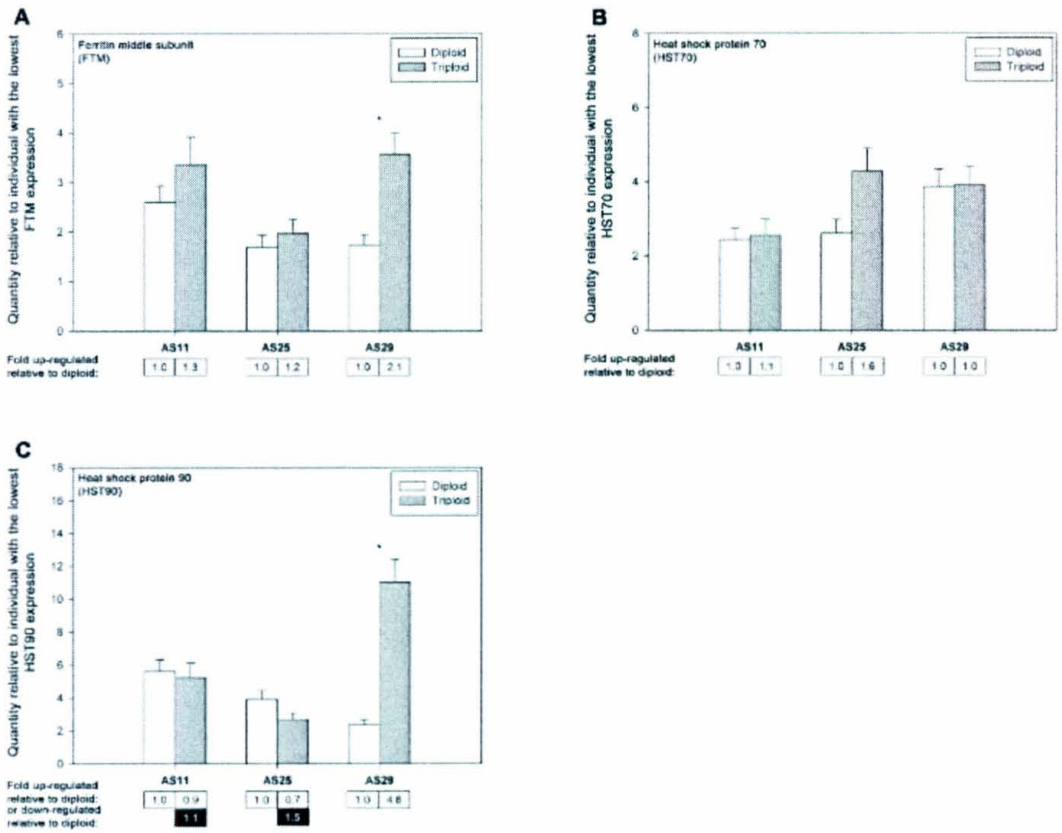
AS25: 2N > 3N (any 3 out of 4 slides): 17 microarray features (Appendix IX)
3N > 2N (any 3 out of 4 slides): 18 microarray features (Appendix X)



AS29: 2N > 3N (any 3 out of 4 slides): 124 microarray features (Appendix XI)
3N > 2N (any 3 out of 4 slides): 444 microarray features (Appendix XII)



APPENDIX XV. Supplemental figure showing QPCR results for genes of interest selected from the 32K cDNA microarray the 2N vs. 3N study. Relative quantity with associated standard error was determined to demonstrate relative gene expression level among three GH transgenic families: AS11, AS25 and AS29. Difference of expression level between families for a single gene of interest was indicated by p value with a significance cutoff of 0.05 ($p < 0.05$, significant difference, indicated as asterisks; $p \geq 0.05$, no significant difference, indicated as values).


A
Ferritin middle subunit
(FTM)
Diploid
Triploid
Quantity relative to individual with the lowest FTM expression
AS11
AS25
AS29
Fold up-regulated relative to diploid:
1.0 1.3
1.0 1.2
1.0 2.1
B
Heat shock protein 70
(HST70)
Diploid
Triploid
Quantity relative to individual with the lowest HST70 expression
AS11
AS25
AS29
Fold up-regulated relative to diploid:
1.3 1.1
1.0 1.6
1.0 1.0
C
Heat shock protein 90
(HST90)
Diploid
Triploid
Quantity relative to individual with the lowest HST90 expression
AS11
AS25
AS29
Fold up-regulated relative to diploid:
or down-regulated relative to diploid:
1.0 0.9
1.1
1.0 0.7
1.5
1.0 4.6